

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:30:54 ; Search time 1527.67 Seconds
(without alignments)
566.880 Million cell updates/sec

Title: US-09-310-844c-24

Perfect score: 29
Sequence: 1 uagauuuuuuuuagccuaggggcu 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 375216

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estm:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.2	55.9	57	9	AI561770
2	16.2	55.9	77	14	CB262321
3	16	55.2	77	28	BH252676
4	15.4	53.1	61	29	CG590967

66	29	TA123H02P
73	12	BM568281
41	14	CB210991
63	29	EX533881
69	29	CG732697
25	28	AZ993079
60	10	BE871815
51	60	BE871815
64	29	EX003595
66	14	CD925111
69	12	BM128463
72	28	BZ763921
72	29	TA185E01P
73	28	AZ775013
74	9	AI819570
76	9	AA975663
76	12	BI963697
76	28	AZ657549
77	29	CG549254
49	29	BX287070
52	12	BG236504
62	28	BH911891
63	29	CG563472
64	9	AI139668
64	28	AZ808107
66	28	AZ40181
73	12	BI865610
73	29	EX001193
79	14	D11626
31	28	BH910631
43	28	AZ597048
44	29	AL771575
54	12	BI863449
60	9	AL595218
63	12	BG362434
65	29	CG664319
67	9	AI584052
67	10	BE027305
67	28	BZ289657
68	29	CG581901
69	10	BE647308
76	9	AI300666
52	10	AM686481
59	28	B00509
61	9	AI138033
67	29	EX004510
70	13	B0063954
72	13	BQ613481
75	29	CG526082
76	29	CG781030
76	29	BX895575
52	10	BP637245
65	12	BI094834
67	9	AA936041
67	28	BH855810
73	14	CD942294
73	14	CD942294
76	29	AL757078
79	28	AQ073107
80	29	AB082353
37	29	AL951243
39	28	BH909815
40	28	BH857340
40	28	BH857342
40	29	CG779591
43	28	AZ484548
55	9	AT005996
55	9	AA276988
64	29	AL770628
65	29	CG507905
65	29	AL763793
66	29	AL767936
67	9	AA506572
67	29	CG588850
70	9	AA922373

AL463084	T. brucei
BM568281	sal02d02
CB210991	OML01271
EX533881	Arabidops
CG732697	1119150C1
AZ993079	2M0277P20
BE871815	601447803
EX003595	Arabidops
CD925111	G750_1150
BM128463	ifl5c05.x
BZ763921	SALX_1227
TA185E01P	
AZ775013	2M0004K20
AI819570	wj91Q08.x
AA975663	cg63f07.s
BI963697	ie63a09.x
AZ657549	1M0533118
CG549254	OST152329
BX287070	Arabidops
BG236504	nal44c06
BH911891	SALK 0727
CG563472	OST186777
AI139668	QC28h07.x
AZ808107	2M0071024
AZ40181	1M0231E10
BI865610	ft22h02.y
EX001193	Arabidops
D11626	HUMOC13G12
BH910631	SALK 0607
AZ597048	1M0410K10
AL771575	Arabidops
BI863449	ft22h02.x
AL595218	AL595218
BG362434	gb72b09.y
CG664319	OST451176
AI584052	ts13b02.x
B00509	CSRL-115b2-
AI300666	qc22a12.x
AM686481	NF038E05N
B00509	CSRL-115b2-
AI138033	ta75g02.x
EX004510	Arabidops
B0063954	fgf_3.M18
BQ613481	rd07h06.y
CG526082	OST102290
CG781030	1123043A0
BX895575	Arabidops
BP637245	NF002F08L
BI094834	EST-CD34N
AA936041	nz53f10.s
BH855810	SALK 0845
CD942294	RBR 27 Ge
AL757078	Arabidops
AQ073107	EP(3)3672
AB082353	Drosophila
AL951243	Arabidops
BH909815	SALK 0561
BH857340	SALK 0764
BH857342	SALK 0764
CG779591	1123034H1
AZ484548	1M0311N02
AT005996	AT005996
AA276988	va25g03.r
AL770628	Arabidops
CG507905	OST58111
AL763793	Arabidops
AL767936	Arabidops
AA506572	nil7d07.s
CG588850	OST240321
AA922373	ok77e01.s

C	78	13.8	47.6	70	9	AA516989	vh89d02.r	151	13.4	46.2	76	12	BG151596	na61h07.
	79	13.8	47.6	71	10	BE320887	NFO28A06R	C 152	13.4	46.2	76	28	BZ290783	BZ290783 SALK_0914
	80	13.8	47.6	72	28	CA458528	SALK_1194	C 153	13.4	46.2	77	10	AW698377	AW698377 G223_glan
	81	13.8	47.6	73	29	CQ507904	OST58109	C 154	13.4	46.2	79	14	W89294	W89294 mf62h03.r1
	82	13.8	47.6	76	29	CG507904	OST58109	C 155	13.2	45.5	28	28	AZ379665	AZ379665 1M0134019
	83	13.8	47.6	77	13	CG656582	OST5429400	C 156	13.2	45.5	33	9	AU256066	AU256066 AU256066
	84	13.8	47.6	77	13	BQ100875	1j25a03.x	C 157	13.2	45.5	34	28	AZ776073	AZ776073 2M0009M20
	85	13.8	47.6	78	9	AL593367	AL593367	C 158	13.2	45.5	34	29	AX001854	AX001854 Arabidops
	86	13.8	47.6	78	14	CK101830	F122P85.5	C 159	13.2	45.5	50	9	AI05680	AI05680 AU105680
	87	13.8	47.6	78	14	CK108462	I018P45.P	C 160	13.2	45.5	52	28	BZ662046	BZ662046 SALK_0255
	88	13.8	47.6	79	29	AL948895	Arabidops	C 161	13.2	45.5	53	28	AZ376460	AZ376460 1M0130017
	89	13.8	47.6	80	29	AL770832	Arabidops	C 162	13.2	45.5	55	28	BZ288871	BZ288871 SALK_0222
	90	13.6	46.9	22	14	D18745	WUGS01807	C 163	13.2	45.5	56	28	AZ938752	AZ938752 2M0137N19
	91	13.6	46.9	39	13	BA556938	BA556938	C 164	13.2	45.5	57	9	AA584628	AA584628 nc12808.8
	92	13.6	46.9	42	14	CF294887	3ODGS--04	C 165	13.2	45.5	58	9	AI824019	AI824019 WJ29f03.x
	93	13.6	46.9	47	9	AU254247	AU254247	C 166	13.2	45.5	59	9	AL930881	AL930881 AU256410
	94	13.6	46.9	49	10	BE970036	BE970036	C 167	13.2	45.5	59	9	AU256410	AU256410 AU256410
	95	13.6	46.9	50	9	AU104386	AU104386	C 168	13.2	45.5	61	12	BI793571	BI793571 1c40H02.X
	96	13.6	46.9	50	12	BT942315	sh06a05.Y	C 169	13.2	45.5	61	29	CG582542	CG582542 OST223810
	97	13.6	46.9	56	28	BA906957	SALK_0368	C 170	13.2	45.5	61	29	CG582542	CG582542 OST223810
	98	13.6	46.9	58	13	BQ586792	E012390-0	C 171	13.2	45.5	62	29	CG523257	CG523257 OST234636
	99	13.6	46.9	58	29	BA906957	Arabidops	C 172	13.2	45.5	62	29	CG559308	CG559308 OST178029
	100	13.6	46.9	61	12	BM123335	L0523C08-	C 173	13.2	45.5	64	9	AI139668	AI139668 Q28h07.X
	101	13.6	46.9	62	10	B8647045	UI-M-BH1-	C 174	13.2	45.5	64	10	AW874915	AW874915 SWYACAL04
	102	13.6	46.9	65	9	AI960274	sc81c01.Y	C 175	13.2	45.5	65	9	AI019809	AI019809 ua93C08.r
	103	13.6	46.9	65	29	CG610825	OST294984	C 176	13.2	45.5	65	14	CD946488	CD946488 REO_34.Ge
	104	13.6	46.9	67	28	AZ760573	1M055124	C 177	13.2	45.5	65	29	CG708273	CG708273 1119008C1
	105	13.6	46.9	67	28	CG458056	SAUK_1154	C 178	13.2	45.5	66	28	AZ471060	AZ471060 1M0285002
	106	13.6	46.9	68	14	CD682098	rj46c08.Y	C 179	13.2	45.5	67	9	AA708911	AA708911 z16a10.8
	107	13.6	46.9	68	28	AZ367374	1M0117805	C 180	13.2	45.5	68	14	CD946488	CD946488 REO_34.Ge
	108	13.6	46.9	72	9	AA682755	ah52f07.s	C 181	13.2	45.5	68	29	CG644709	CG644709 OST388378
	109	13.6	46.9	72	9	AI900474	sc11b10.Y	C 182	13.2	45.5	68	29	CG644709	CG644709 OST388378
	110	13.6	46.9	73	9	AA661115	WZ68h11.X	C 183	13.2	45.5	69	28	AZ456041	AZ456041 1M0258J10
	111	13.6	46.9	73	28	AZ290626	10606020G0	C 184	13.2	45.5	71	9	AA789166	AA789166 ag58b03.s
	112	13.6	46.9	78	12	BM515022	cx95a08.Y	C 185	13.2	45.5	71	29	AG264184	AG264184 Lotus cor
	113	13.4	46.2	34	29	TA98E04P	T. brucei	C 186	13.2	45.5	72	28	AZ776513	AZ776513 2M0010M10
	114	13.4	46.2	45	29	AL761592	Arabidops	C 187	13.2	45.5	74	28	BH789670	BH789670 SALK_0423
	115	13.4	46.2	48	28	BZ596082	SALK_0920	C 188	13.2	45.5	75	12	BG362263	BG362263 g575f05.Y
	116	13.4	46.2	50	9	AI960055	sc37e07.X	C 189	13.2	45.5	75	29	CG618181	CG618181 OST312509
	117	13.4	46.2	50	28	BZ289491	SAUK_0228	C 190	13.2	45.5	75	29	AL754690	AL754690 Arabidops
	118	13.4	46.2	52	9	AU258888	AU258888	C 191	13.2	45.5	76	13	BQ536895	BQ536895 STEM2.18
	119	13.4	46.2	53	10	BF637089	NFO50F04L	C 192	13.2	45.5	76	13	BQ536895	BQ536895 STEM2.18
	120	13.4	46.2	53	29	BE660051	Arabidops	C 193	13.2	45.5	76	13	BQ536895	BQ536895 STEM2.18
	121	13.4	46.2	56	12	BG231426	na142f02.	C 194	13.2	45.5	77	13	BQ52110	BQ52110 1112097E1
	122	13.4	46.2	58	28	B02943	CSRL-16302-	C 195	13.2	45.5	77	29	AL944740	AL944740 Arabidops
	123	13.4	46.2	59	9	AI651430	wa22b08.X	C 196	13.2	45.5	78	9	AA498911	AA498911 v183D06.r
	124	13.4	46.2	59	29	AL766549	Arabidops	C 197	13.2	45.5	78	28	BH252197	BH252197 SALK_0129
	125	13.4	46.2	61	14	CD984792	QAM25f05.	C 198	13.2	45.5	79	14	CD582985	CD582985 x129a04.Y
	126	13.4	46.2	62	10	BF470295	UI-M-BH3-	C 199	13.2	45.5	79	28	AZ336769	AZ336769 1M0067L12
	127	13.4	46.2	63	12	BG362361	gb70h04.Y	C 200	13.2	45.5	80	29	CG474696	CG474696 OST2739.M
	128	13.4	46.2	63	14	CB9312680	rj05g06.Y	C 201	13.4	44.8	27	2	HS0003610	HS0003610 Homo sapi
	129	13.4	46.2	63	29	CG598869	OST264706	C 202	13.4	44.8	27	28	BH909838	BH909838 SALK_0561
	130	13.4	46.2	64	9	AA935784	vz35h02.X	C 203	13.4	44.8	29	29	TA294B05P	TA294B05P Homo sapi
	131	13.4	46.2	64	28	AZ509948	1M0354E07	C 204	13.4	44.8	30	2	HS0001042	HS0001042 Homo sapi
	132	13.4	46.2	64	29	BA291940	Arabidops	C 205	13.4	44.8	30	2	HS0001581	HS0001581 Homo sapi
	133	13.4	46.2	65	9	AA620913	af96b03.s	C 206	13.4	44.8	32	2	HS0001595	HS0001595 Homo sapi
	134	13.4	46.2	67	13	BT761969	BT761969	C 207	13.4	44.8	32	2	HS0001674	HS0001674 Homo sapi
	135	13.4	46.2	67	14	CB165153	86 Alfalf	C 208	13.4	44.8	33	2	HS0003086	HS0003086 Homo sapi
	136	13.4	46.2	69	9	AI211081	n0e06al.f	C 209	13.4	44.8	33	2	HS0003165	HS0003165 Homo sapi
	137	13.4	46.2	70	9	AI609394	FW93203.X	C 210	13.4	44.8	33	9	AL048719	AL048719 DKEP2566G
	138	13.4	46.2	70	9	AV916602	AV916602	C 211	13.4	44.8	33	9	AL048733	AL048733 DKEP2566G
	139	13.4	46.2	71	12	BM873635	laa01a12.	C 212	13.4	44.8	34	2	HS0003069	HS0003069 Homo sapi
	140	13.4	46.2	71	14	CK109829	N029E03.P	C 213	13.4	44.8	34	2	HS0001818	HS0001818 Homo sapi
	141	13.4	46.2	72	13	BU744002	mah94e12.	C 214	13.4	44.8	42	28	BZ661965	BZ661965 SALK_0254
	142	13.4	46.2	72	28	AZ760023	1M0553F22	C 215	13.4	44.8	42	28	AZ637149	AZ637149 1M0496F19
	143	13.4	46.2	72	29	CG780334	11203039A0	C 216	13.4	44.8	44	9	AU008189	AU008189 Arabidops
	144	13.4	46.2	73	12	BM889450	laa01a12.	C 217	13.4	44.8	44	29	AL753209	AL753209 Arabidops
	145	13.4	46.2	74	28	AZ986310	2M0268024	C 218	13.4	44.8	46	9	AI103611	AI103611 tw65a03.X
	146	13.4	46.2	74	28	BH642955	100805080	C 219	13.4	44.8	46	9	AI103611	AI103611 tw65a03.X
	147	13.4	46.2	74	29	CG574740	OST207881	C 220	13.4	44.8	50	29	AL752392	AL752392 Arabidops
	148	13.4	46.2	74	29	CG723421	1119076C1	C 221	13.4	44.8	52	10	AW245287	AW245287 2820140.3
	149	13.4	46.2	75	14	H07686	kg8e012.BNL	C 222	13.4	44.8	53	10	AW245287	AW245287 2820140.3
	150	13.4	46.2	75	28	AZ453746	1M0255A23	C 223	13.4	44.8	54	29	CC886314	CC886314 SALK_1516

C 370	12.6	43.4	55	9	AI913058	AI913058 tz75f07.x	C 443	12.4	42.8	45	29	AG206278	AG206278 Oryza sat
C 371	12.6	43.4	57	9	AU252594	AU252594 AU252594	C 444	12.4	42.8	46	28	AZ833686	AZ833686 2M0115L20
C 372	12.6	43.4	57	13	BX553132	BX553132 BX553132	C 445	12.4	42.8	49	9	AA846570	AA846570 aj97c02.s
C 373	12.6	43.4	57	28	BH849364	BH849364 SALK_0695	C 446	12.4	42.8	49	10	AW334086	AW334086 S30C3 AGS
C 374	12.6	43.4	57	28	BH850801	BH850801 SALK_0718	C 447	12.4	42.8	49	14	CF321218	CF321218 HD--12-GO
C 375	12.6	43.4	58	9	AU010373	AU010373 AU010373	C 448	12.4	42.8	49	14	W96814	W96814 zb61f02.r1
C 376	12.6	43.4	58	14	CB274954	CB274954 ku73d01.y	C 449	12.4	42.8	50	29	AL945912	AL945912 Arabidops
C 377	12.6	43.4	58	28	BH904512	BH904512 SALK_1045	C 450	12.4	42.8	51	28	B01106	B01106 CSR1-125312
C 378	12.6	43.4	61	9	AI650326	AI650326 wai8e08.x	C 451	12.4	42.8	52	9	AI540848	AI540848 tp86c11.x
C 379	12.6	43.4	61	9	AA554915	AA554915 nk31e06.s	C 452	12.4	42.8	52	9	AI697308	AI697308 tq07f02.x
C 380	12.6	43.4	61	9	AA595454	AA595454 no34d06.s	C 453	12.4	42.8	52	9	AU256791	AU256791 AU256791
C 381	12.6	43.4	61	14	CF053677	CF053677 QCN1b04.y	C 454	12.4	42.8	52	9	AI224228	AI224228 QX26609.x
C 382	12.6	43.4	61	29	CS510250	CS510250 QST61872	C 455	12.4	42.8	53	13	BX562212	BX562212 BX562212
C 383	12.6	43.4	62	9	AV365244	AV365244 AV365244	C 456	12.4	42.8	53	28	BH910562	BH910562 SALK_0637
C 384	12.6	43.4	62	29	CD401366	CD401366 Gm CK2346	C 457	12.4	42.8	54	29	BX001821	BX001821 Arabidops
C 385	12.6	43.4	63	14	CD401366	CD401366 Gm CK2346	C 458	12.4	42.8	54	29	BX001821	BX001821 Arabidops
C 386	12.6	43.4	64	9	AI670974	AI670974 wb12f03.x	C 459	12.4	42.8	55	2	HS0001638	HS0001638 Homo sapi
C 387	12.6	43.4	64	9	AA594204	AA594204 nn39d04.s	C 460	12.4	42.8	55	9	AI913453	AI913453 tz77609.x
C 388	12.6	43.4	64	14	CF017541	CF017541 QBM25e10.	C 461	12.4	42.8	55	9	BE321082	BE321082 NF033G05R
C 389	12.6	43.4	65	12	BN898426	BN898426 p65a05.y	C 462	12.4	42.8	55	29	AL760223	AL760223 Arabidops
C 390	12.6	43.4	65	29	CS545761	CS545761 CBT146689	C 463	12.4	42.8	55	29	AL760223	AL760223 Arabidops
C 391	12.6	43.4	66	29	AG260513	AG260513 Lotus cor	C 464	12.4	42.8	56	12	BI491371	BI491371 df07h12.w
C 392	12.6	43.4	67	9	AA894821	AA894821 cf61d12.s	C 465	12.4	42.8	56	12	BM445434	BM445434 L1L11C9.a
C 393	12.6	43.4	67	9	AI917918	AI917918 tz14f06.x	C 466	12.4	42.8	56	13	BQ787611	BQ787611 tm13b12.x
C 394	12.6	43.4	67	13	B0075738	B0075738 fz08c12.y	C 467	12.4	42.8	57	12	BG235467	BG235467 NCBST3A36
C 395	12.6	43.4	67	14	CB261630	CB261630 93-E8866-	C 468	12.4	42.8	57	28	AZ657854	AZ657854 1M0534L15
C 396	12.6	43.4	67	14	CB953649	CB953649 SB1_4 Gen	C 469	12.4	42.8	57	28	AZ657854	AZ657854 1M0534L15
C 397	12.6	43.4	69	29	CNS052UP	AI182554 Tetradon	C 470	12.4	42.8	57	28	AZ782127	AZ782127 2M0022B08
C 398	12.6	43.4	70	9	AA931825	AA931825 om83a06.s	C 471	12.4	42.8	58	9	AI709231	AI709231 at01f04.x
C 399	12.6	43.4	70	9	AL780467	AL780467 AL780467	C 472	12.4	42.8	58	28	AZ834846	AZ834846 2M0117P18
C 400	12.6	43.4	70	14	CB359615	CB359615 ZF001-P00	C 473	12.4	42.8	58	28	BH789684	BH789684 SALK_0444
C 401	12.6	43.4	71	12	BN898279	BN898279 ph62f08.y	C 474	12.4	42.8	60	9	AI539048	AI539048 tp76h01.x
C 402	12.6	43.4	71	28	AZ786367	AZ786367 2M0031016	C 475	12.4	42.8	60	9	AI719784	AI719784 as41h08.x
C 403	12.6	43.4	71	29	CNS02ABD	AI188338 Tetradon	C 476	12.4	42.8	60	9	AU268022	AU268022 AU268022
C 404	12.6	43.4	72	10	BR977483	BR977483 b654e10.y	C 477	12.4	42.8	60	9	AW020312	AW020312 df07h12.y
C 405	12.6	43.4	73	12	BG621583	BG621583 602611180	C 478	12.4	42.8	60	29	CC793054	CC793054 SALK_0074
C 406	12.6	43.4	73	14	CD960600	CD960600 SDE_274 G	C 479	12.4	42.8	63	14	CF806791	CF806791 psH0162A
C 407	12.6	43.4	73	29	CG529491	CG529491 OST109956	C 480	12.4	42.8	63	28	BH415899	BH415899 1007044D0
C 408	12.6	43.4	73	29	CG664820	CG664820 OST452459	C 481	12.4	42.8	64	10	BF118524	BF118524 NF037B11L
C 409	12.6	43.4	74	9	AL660462	AL660462 AL660462	C 482	12.4	42.8	64	10	BF118524	BF118524 SMOVL3CAN
C 410	12.6	43.4	74	28	B2357883	B2357883 SALK_1314	C 483	12.4	42.8	64	10	BF219632	BF219632 SMOVL3CAN
C 411	12.6	43.4	75	9	AI696772	AI696772 wc61d07.x	C 484	12.4	42.8	64	10	BF219632	BF219632 SMOVL3CAN
C 412	12.6	43.4	75	9	AA598953	AA598953 ae37h08.s	C 485	12.4	42.8	64	10	BF219632	BF219632 SMOVL3CAN
C 413	12.6	43.4	75	9	AA615120	AA615120 vm02b09.r	C 486	12.4	42.8	65	9	AI281558	AI281558 QJ5202.x
C 414	12.6	43.4	75	10	BE223726	BE223726 kp88a10.y	C 487	12.4	42.8	65	28	BH908271	BH908271 SALK_0468
C 415	12.6	43.4	75	28	BH910959	BH910959 SALK_0636	C 488	12.4	42.8	65	29	FR0053439	FR0053439 Fugu rubr
C 416	12.6	43.4	75	28	CG179654	CG179654 SALK_0719	C 489	12.4	42.8	65	29	FR0053439	FR0053439 Fugu rubr
C 417	12.6	43.4	75	29	CG520478	CG520478 CH240_367	C 490	12.4	42.8	66	12	BG361618	BG361618 gb55g07.y
C 418	12.6	43.4	75	29	AG218208	AG218208 Drosophi	C 491	12.4	42.8	66	12	BG361618	BG361618 gb55g07.y
C 419	12.6	43.4	76	9	AI316047	AI316047 uj61g05.y	C 492	12.4	42.8	66	12	CF115732	CF115732 SSF508E18
C 420	12.6	43.4	76	9	AU011284	AU011284 AU011284	C 493	12.4	42.8	66	28	AZ787829	AZ787829 2M0255L09
C 421	12.6	43.4	76	28	BZ289518	BZ289518 SALK_0229	C 494	12.4	42.8	66	29	CG646385	CG646385 OST192574
C 422	12.6	43.4	76	29	CG475280	CG475280 OST3535.M	C 495	12.4	42.8	67	9	AA659476	AA659476 nu25a09.s
C 423	12.6	43.4	77	14	CB263298	CB263298 66-E9721-	C 496	12.4	42.8	67	9	AI311273	AI311273 ta48h07.x
C 424	12.6	43.4	77	14	R38641	R38641 vt59b10.r1	C 497	12.4	42.8	67	9	AI921937	AI921937 wt86h08.x
C 425	12.6	43.4	77	29	CG899207	CG899207 01S0620-0	C 498	12.4	42.8	68	13	BX708928	BX708928 Arabidops
C 426	12.6	43.4	78	9	AA334074	AA334074 on78d07.s	C 499	12.4	42.8	69	29	AI950439	AI950439 Arabidops
C 427	12.6	43.4	78	28	BH904967	BH904967 SALK_1054	C 500	12.4	42.8	69	29	AI950439	AI950439 Arabidops
C 428	12.6	43.4	79	29	AL951473	AL951473 Arabidops	C 501	12.4	42.8	70	14	CB935228	CB935228 Arabidops
C 429	12.6	43.4	80	29	BX662420	BX662420 Arabidops	C 502	12.4	42.8	70	28	BH850759	BH850759 SALK_0718
C 430	12.4	42.8	80	28	BH790181	BH790181 SALK_0565	C 503	12.4	42.8	70	29	CG795791	CG795791 SALK_0883
C 431	12.4	42.8	80	28	AZ416940	AZ416940 1M0152H21	C 504	12.4	42.8	71	13	BQ692851	BQ692851 pt07h05.y
C 432	12.4	42.8	80	28	AU259110	AU259110 AU259110	C 505	12.4	42.8	71	13	BQ692851	BQ692851 pt07h05.y
C 433	12.4	42.8	80	28	BF032106	BF032106 601555966	C 506	12.4	42.8	71	13	BQ692851	BQ692851 pt07h05.y
C 434	12.4	42.8	80	14	CF032089	CF032089 7LEAF--08	C 507	12.4	42.8	71	13	BQ692851	BQ692851 pt07h05.y
C 435	12.4	42.8	80	14	AU011968	AU011968 AU011968	C 508	12.4	42.8	71	28	BH789678	BH789678 SALK_0444
C 436	12.4	42.8	80	9	AU011969	AU011969 AU011969	C 509	12.4	42.8	71	28	BH789678	BH789678 SALK_0444
C 437	12.4	42.8	80	9	AU011971	AU011971 AU011971	C 510	12.4	42.8	71	28	BH789678	BH789678 SALK_0444
C 438	12.4	42.8	80	9	AU011973	AU011973 AU011973	C 511	12.4	42.8	71	28	BH789678	BH789678 SALK_0444
C 439	12.4	42.8	80	28	BH852384	BH852384 SALK_0745	C 512	12.4	42.8	71	29	CG545852	CG545852 OST144556
C 440	12.4	42.8	80	28	BZ352392	BZ352392 SALK_0789	C 513	12.4	42.8	71	29	CG545852	CG545852 OST144556
C 441	12.4	42.8	80	28	BX659541	BX659541 Arabidops	C 514	12.4	42.8	73	10	BF123392	BF123392 601759189
C 442	12.4	42.8	80	28	BH808431	BH808431 100807991	C 515	12.4	42.8	73	14	CD866433	CD866433 AZ02.103G

516 12.4 42.8 73 14 U44288 U44288 ENU44288 AS
C 517 12.4 42.8 74 9 AI379808 tb91c04.x
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C 519 12.4 42.8 75 9 AI307206 AI307206 tb36h07.x
520 12.4 42.8 75 12 BI703772 BI703772 Kx20912.Y
521 12.4 42.8 75 12 BM571633 BM571633 fx04a07.x
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525 12.4 42.8 76 9 AI633915 AI633915 tt23a07.x
C 526 12.4 42.8 76 9 AW059618 AW059618 HUTH.bs8t
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530 12.4 42.8 77 10 AW516108 AW516108 xt60h07.x
C 531 12.4 42.8 78 9 AA936218 AA936218 on43c01.x
532 12.4 42.8 78 9 AI252514 AI252514 QV30c11.x
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C 535 12.2 42.1 31 28 AZ997553 AZ997553 2M0284E10
536 12.2 42.1 33 28 BH740759 BH740759 KGO1661-3
C 537 12.2 42.1 33 28 BH791695 BH791695 SALK_0608
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C 539 12.2 42.1 38 29 DM545254 DM545254 Drosophila
540 12.2 42.1 39 28 BH840522 BH840522 KGO3386-5
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542 12.2 42.1 40 28 AZ815739 AZ815739 2M0084K13
C 543 12.2 42.1 42 9 AI833018 AI833018 at74c04.x
544 12.2 42.1 43 9 AI758314 AI758314 ty06c01.x
C 545 12.2 42.1 43 29 AL766396 AL766396 Arabidops
546 12.2 42.1 44 29 BX121347 BX121347 Danio rer
C 547 12.2 42.1 45 28 BH853902 BH853902 SALK_0784
548 12.2 42.1 46 9 AI624478 AI624478 t68e05.x
C 549 12.2 42.1 46 28 BH792322 BH792322 SALK_0634
550 12.2 42.1 47 29 AL756982 AL756982 Arabidops
C 551 12.2 42.1 47 29 TA92D04Q TA92D04Q T. brucei
552 12.2 42.1 48 28 BH901374 BH901374 SALK_0786
C 553 12.2 42.1 49 9 AV960827 AV960827 HUMGS000333
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556 12.2 42.1 49 29 BX649704 BX649704 Arabidops
C 557 12.2 42.1 49 29 BX893214 BX893214 Arabidops
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C 569 12.2 42.1 53 12 BM891460 BM891460 sam27f03.
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574 12.2 42.1 54 28 BH234921 BH234921 MHAA_C04
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C 579 12.2 42.1 56 13 C21299 C21299 HUMGS000237
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593 12.2 42.1 59 28 BZ595463 BZ595463 SALK_0870
C 594 12.2 42.1 59 29 AI758356 AI758356 Arabidops
595 12.2 42.1 61 9 AI440824 AI440824 ea8e11.Y
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597 12.2 42.1 61 28 BZ289575 BZ289575 SALK_0229
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599 12.2 42.1 62 9 AA026245 AA026245 zj99a02.s
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601 12.2 42.1 62 9 AL944090 AL944090 Arabidops
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603 12.2 42.1 63 12 EG361068 EG361068 gb45e09.Y
C 604 12.2 42.1 63 28 BZ597224 BZ597224 SALK_1005
605 12.2 42.1 64 9 AI570111 AI570111 tr74d11.x
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C 608 12.2 42.1 64 10 AA409544 AA409544 SVOV3WCAM
609 12.2 42.1 64 10 BB638296 BB638296 SVOV3WCAM
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613 12.2 42.1 64 14 D20622 D20622 HUMGS01597
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619 12.2 42.1 64 29 TA121E03P TA121E03P T. brucei
C 620 12.2 42.1 65 9 AA208741 AA208741 mu65d06.r
621 12.2 42.1 65 10 AW423329 AW423329 sh66c03.Y
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623 12.2 42.1 65 14 CD943324 CD943324 RCO_26.Ge
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637 12.2 42.1 67 9 AI936499 AI936499 wd28f07.x
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639 12.2 42.1 67 14 CD966066 CD966066 SEL_513.G
C 640 12.2 42.1 67 28 BH909420 BH909420 SALK_0535
641 12.2 42.1 68 9 AI880472 AI880472 at78c12.x
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649 12.2 42.1 70 13 BQ480126 BQ480126 faa86d04.
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659 12.2 42.1 72 28 BZ596806 BZ596806 SALK_0360
C 660 12.2 42.1 72 28 BZ661345 BZ661345 SALK_0248
661 12.2 42.1 72 28 BZ661345 BZ661345 SALK_0248

AV739274 AV739274
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BQ479345 ku3d12.Y
BZ289575 SALK_0229
CG666107 OST455751
AA026245 zj99a02.s
AI481932 vH86d11.x
AL944090 Arabidops
BX165948 Danio rer
EG361068 gb45e09.Y
BZ597224 SALK_1005
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AA409544 SVOV3WCAM
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AZ775161 2M0007F15
BH811901 SALK_0604
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CG629148 OST40948
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CD943324 RCO_26.Ge
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CG785992 98F0079-0
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A2623479 1M0461116
CG556234 OST171625
CG570250 OST198988
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CD966066 SEL_513.G
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BU576112 Tgs8TzyD8
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AZ649694 1M0519N24
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663	12.2	42.1	73	9	AI330688	AI330688 fa91g03.y	C 736	12	41.4	52	14	T83359	T83359 y82d08.s1
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665	12.2	42.1	73	12	BI107307	BI107307 602894328	C 738	12	41.4	52	29	AB081935	AB081935 Drosophi1
666	12.2	42.1	73	29	AI771410	AI771410 Arabidops	C 739	12	41.4	52	29	TA121B12Q	TA121B12Q T. brucei
667	12.2	42.1	74	13	BQ275575	BQ275575 D336f10.y	C 740	12	41.4	53	9	AL790756	AL790756 AL790756
668	12.2	42.1	74	14	CD913649	CD913649 G608.114B	C 741	12	41.4	53	28	B01982	B01982 CSRL-144H11
669	12.2	42.1	74	29	AI767013	AI767013 Arabidops	C 742	12	41.4	53	28	B01982	B01982 CSRL-144H11
670	12.2	42.1	75	9	AI938927	AI938927 sc63a02.y	C 743	12	41.4	54	28	B01982	B01982 CSRL-144H11
671	12.2	42.1	75	13	BH078450	BH078450 V047D08.P	C 744	12	41.4	54	28	B01982	B01982 CSRL-144H11
672	12.2	42.1	75	14	CK098783	CK098783 A031P73.5	C 745	12	41.4	54	28	B01982	B01982 CSRL-144H11
673	12.2	42.1	75	28	BK040857	BK040857 1007005C0	C 746	12	41.4	56	28	AL695651	AL695651 1M0204KL5
674	12.2	42.1	75	28	BH911917	BH911917 SALK_0730	C 747	12	41.4	56	29	CG799256	CG799256 1118001B0
675	12.2	42.1	75	29	CG475700	CG475700 OS4213.M	C 748	12	41.4	56	29	CG799256	CG799256 1118001B0
676	12.2	42.1	76	29	BX203424	BX203424 Dario rer	C 749	12	41.4	57	13	BX778267	BX778267 BX778267
677	12.2	42.1	76	9	AA502239	AA502239 ne94d05.s	C 750	12	41.4	57	13	BX778267	BX778267 BX778267
678	12.2	42.1	76	10	AW194637	AW194637 xn42g04.x	C 751	12	41.4	58	9	AI584456	AI584456 fb93h12.x
679	12.2	42.1	76	10	BH867849	BH867849 601433622	C 752	12	41.4	58	9	AI584456	AI584456 fb93h12.x
680	12.2	42.1	76	28	AQ025263	AQ025263 EP(13)3081	C 753	12	41.4	59	13	BQ524737	BQ524737 NISC no06
681	12.2	42.1	76	28	B2380384	B2380384 SALK_1150	C 754	12	41.4	59	13	BQ524737	BQ524737 NISC no06
682	12.2	42.1	76	29	CG558835	CG558835 OS7435402	C 755	12	41.4	60	9	AI949039	AI949039 wg36c03.x
683	12.2	42.1	76	29	CG706108	CG706108 0180707-0	C 756	12	41.4	60	9	AI949039	AI949039 wg36c03.x
684	12.2	42.1	76	29	BX532742	BX532742 Arabidops	C 757	12	41.4	60	14	CB410162	CB410162 NISC no09
685	12.2	42.1	77	9	AL866175	AL866175 Arabidops	C 758	12	41.4	60	14	CB410162	CB410162 NISC no09
686	12.2	42.1	77	10	AW700694	AW700694 pa43b07.y	C 759	12	41.4	61	9	AI000397	AI000397 ot06e12.s
687	12.2	42.1	77	28	AF067770	AF067770 AF067770	C 760	12	41.4	61	9	AI000397	AI000397 ot06e12.s
688	12.2	42.1	77	28	AZ982711	AZ982711 2M0263C07	C 761	12	41.4	61	28	BH863498	BH863498 SALK_0940
689	12.2	42.1	77	29	CG479385	CG479385 ST10166	C 762	12	41.4	61	28	BH863498	BH863498 SALK_0940
690	12.2	42.1	77	29	CG610667	CG610667 OS2294349	C 763	12	41.4	62	29	CG475777	CG475777 OST139482
691	12.2	42.1	77	29	AL763184	AL763184 Arabidops	C 764	12	41.4	62	29	CG475777	CG475777 OST139482
692	12.2	42.1	78	9	AL854995	AL854995 Arabidops	C 765	12	41.4	62	29	CG475777	CG475777 OST139482
693	12.2	42.1	78	10	BF438294	BF438294 7q07e06.x	C 766	12	41.4	63	29	CG475777	CG475777 OST139482
694	12.2	42.1	78	13	BQ244462	BQ244462 TAEL5037B	C 767	12	41.4	63	29	CG475777	CG475777 OST139482
695	12.2	42.1	78	28	BH810230	BH810230 SALK_0482	C 768	12	41.4	64	10	BE318106	BE318106 SALK_0482
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707	12.2	42.1	80	14	CF043983	CF043983 QCU23909.	C 780	12	41.4	66	12	BJ079690	BJ079690 BJ079690
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718	12.2	42.1	80	29	BH850881	BH850881 SALK_0720	C 791	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
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725	12.2	42.1	80	29	AL771654	AL771654 Arabidops	C 798	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
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727	12.2	42.1	80	29	BZ765916	BZ765916 SALK_1355	C 800	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
728	12.2	42.1	80	29	AU104264	AU104264 AU104264	C 801	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
729	12.2	42.1	80	29	AU107304	AU107304 AU107304	C 802	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
730	12.2	42.1	80	29	BQ370398	BQ370398 nai33a04.	C 803	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
731	12.2	42.1	80	29	AQ026078	AQ026078 l(2)k1440	C 804	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
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C 816	12	41.4	71	28	BH846325	SALK_0072	C 889	11.8	40.7	40	13	BX554624
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C 823	12	41.4	73	29	BX653912	ArabiDops	C 896	11.8	40.7	46	9	AA131380
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C 825	12	41.4	74	29	TA57C05P	ArabiDops	C 898	11.8	40.7	47	10	AH333805
C 826	12	41.4	75	9	AW733972	v21h10.r	C 899	11.8	40.7	47	28	BH620060
C 827	12	41.4	75	28	BH855879	SALK_0844	C 900	11.8	40.7	47	28	BH910648
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C 834	12	41.4	76	28	BZ289798	SALK_0232	C 907	11.8	40.7	49	28	BH911354
C 835	12	41.4	76	29	CG616155	OST307956	C 908	11.8	40.7	49	28	CC049611
C 836	12	41.4	77	9	A1669640	tw34g09.x	C 909	11.8	40.7	49	29	PCH303697
C 837	12	41.4	77	9	AL897168	AL897168	C 910	11.8	40.7	50	9	AI241767
C 838	12	41.4	77	9	AW025775	wu07G03.x	C 911	11.8	40.7	50	9	AU255886
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ALIGNMENTS

RESULT 1
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 LOCUS v65b08.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
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 ACCESSION AI561770
 VERSION AI561770.1 GI:4513115
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 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 57)
 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
 Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Willson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Contact: Marra M/WashU-NCI Mouse EST Project 1999
 COMMENT

FEATURES
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 Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
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 adaptor sequence: 5' GAATCGCAGCAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 55.9%; Score 16.2; DB 9; Length 57;
 Best Local Similarity 37.9%; Pred. No. 7.6e+04;
 Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy

1 UAUAUUCUUUUUUAAGCCUAGGGGCU 29

Db

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RESULT 2

CB262321 77 bp mRNA linear EST 06-NOV-2003
 66-B8967-008-015-C18-PB12 MP1Z-ADIS-008 Arabidopsis thaliana cDNA
 clone MP1Zp767C1815Q 5-PRIME, mRNA sequence.

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

TITLE

Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 77 Std Error: 0.00
 Plate: 15 row: C column: 18
 Seq primer: PB12; GGTGGCGCCGCTCTAG.
 Location/Qualifiers
 1..77
 /organism="Arabidopsis thaliana"

FEATURES

source

```

/mol_type="mRNA"
/cultivar="C24"
/db_xref="GABI:600707"
/db_xref="taxon:3702"
/clone="MPIZp767C1815Q"
/tissue_type="seedling"
/dev_stage="few days old seedlings"
/lab_host="E. coli XL1-Blue MRF"
/clone_lib="MPIZ-ADIS-008"
/notes="Vector: pBluescript SK (-); Site 1: EcoRI; Site 2:
XhoI; cDNA library from Arabidopsis thaliana, accession
C24; seedling: Lambda ZAPII phage library was made at the
Max-Planck-Institute of Molecular Plant Physiology, Goltm,
Germany and mass-excised at the Max-Planck-Institute for
Plant Breeding Research, Cologne, Germany; cloning sites
EcoRI-XhoI; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Etablissement of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' Pt: Bernd Weisshaar Sequence submission Managed
by RZPD/GABI-Primary database; http://gabi.rzpd.de This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

```

ORIGIN

```

Query Match      55.9%; Score 16.2; DB 14; Length 77;
Best Local Similarity 37.9%; Pred. No. 7.3e+04;
Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy 1 UAGAUUUUUUUUUAAGCCUAGGGGCU 29
   : : : : : : : : : : : : : : : :
Db 22 TTTTITTTTTTTTGAACCAACCGGGGTT 50

```

RESULT 3

```

BH252676      77 bp DNA linear GSS 28-NOV-2001
LOCUS          SAUK_013733 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION     thaliana genomic clone SAUK_013733, genomic survey sequence.
ACCESSION      BH252676
VERSION        BH252676.1 GI:17139654
KEYWORDS
SOURCE

```

ORGANISM

```

Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

```

REFERENCE

```

1 (bases 1 to 77)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmermann, J., and Ecker, J.R.

```

```

A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

```

UNPUBLISHED (2001)

```

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

```

```

This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

```

FEATURES

```

source
1..77
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAUK_013733"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines

```

```

each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

```

ORIGIN

```

Query Match      55.2%; Score 16; DB 28; Length 77;
Best Local Similarity 43.8%; Pred. No. 8.6e+04;
Matches 7; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AUGAUUUUUUUUUUA 17
   : : : : : : : : : : : : : : : :
Db 10 ATGATTCCTTTTGTAA 25

```

RESULT 4

```

CG590967      61 bp DNA linear GSS 02-OCT-2003
LOCUS          OST245023 Mus musculus 129Sv/Ev Mus musculus genomic clone
DEFINITION     OST245023, genomic survey sequence.
ACCESSION      CG590967
VERSION        CG590967.1 GI:37398378
KEYWORDS
SOURCE

```

ORGANISM

```

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE

```

1 (bases 1 to 61)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Figgott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.

```

```

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

```

JOURNAL

```

COMMENT

```

FEATURES

```

source
1..61
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST245023"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

```

ORIGIN

```

Query Match      53.1%; Score 15.4; DB 29; Length 61;
Best Local Similarity 50.0%; Pred. No. 1.5e+05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 3 UGAUUCUUUUUUAAGCCUAGGGGC 28
   : : : : : : : : : : : : : : : :
Db 58 TGAGCCTTTTTCAGCCCTAGTGCC 33

```

RESULT 5

```

TA123H02P/c
LOCUS          T. brucei sheared genomic DNA clone 123h02, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION      AL463084

```

```

VERSION      AL463084.1  GI:11833690
KEYWORDS     GSS
SOURCE       Trypanosoma brucei
ORGANISM     Trypanosoma brucei
              Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
              Trypanosoma.
REFERENCE    1 (bases 1 to 66)
AUTHORS      Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
              Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
              Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nhelayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.
              Location/Qualifiers
FEATURES             source
     .
     /organism="Trypanosoma brucei"
     /mol_type="genomic DNA"
     /strain="TREU927"
     /db_xref="taxon:5691"
     /clone="123h02"

ORIGIN
Query Match      53.1%; Score 15.4; DB 29; Length 66;
Best Local Similarity 36.0%; Pred. No. 1.5e+05;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY  1 UAUGAUUCUUUUUGUAGCCCUAGG 25
    :|:::|:::|:::|:::|:::|
Db   30 TATGATTTTTCAGACCCCTAAG 6

RESULT 6
BM568281
LOCUS      sa102d02.y1 Gm-cl057 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION 73 bp mRNA linear EST 21-FEB-2002
ACCESSION  BM568281
VERSION     BM568281.1 GI:18849172
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
ORGANISM    Glycine max

REFERENCE
AUTHORS      Shoenaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvett, V.,
              Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
              Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
              Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
              Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
              McCann, R., Waterston, R. and Wilson, R.
              Public Soybean EST Project
              Unpublished (1999)
              Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800

QY  1 UAUGAUUCUUUUUGUAGCCCUAGG 25
    :|:::|:::|:::|:::|:::|
Db   30 TATGATTTTTCAGACCCCTAAG 6

RESULT 7
CB210991/c
LOCUS      OML01271 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',
DEFINITION 41 bp mRNA linear EST 05-FEB-2003
ACCESSION  CB210991
VERSION     CB210991.1 GI:28257082
KEYWORDS    EST.
SOURCE      Oryza minuta
ORGANISM    Oryza minuta
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
              1 (bases 1 to 41)
              Shin, J.S.
              Oryza minuta HybridZAP-2.1 XR library
              Unpublished (2003)
              Contact: Jeong Sheop Shin
              Plant Molecular Genetics
              Graduate School of Biotechnology, University of Korea
              136-701 Anan-dong 5/1 Seoul, Korea
              Tel: 00 82 2 3290 3430
              Fax: 00 82 2 927 9028
              Email: jsshin@kucn.korea.ac.kr.
              Location/Qualifiers
FEATURES             source
     .
     /organism="Oryza minuta"
     /mol_type="mRNA"
     /db_xref="taxon:63629"
     /dev_stage="4-weeks after germination"
     /clone_lib="Oryza minuta HybridZAP-2.1 XR library"

QY  1 UAUGAUUCUUUUUGUAGCCCUAGG 25
    :|:::|:::|:::|:::|:::|
Db   19 TAAGCTTCCTTATTATAACCCAGG 43

Query Match      53.1%; Score 15.4; DB 12; Length 73;
Best Local Similarity 44.0%; Pred. No. 1.5e+05;
Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY  1 UAUGAUUCUUUUUGUAGCCCUAGG 25
    :|:::|:::|:::|:::|:::|
Db   19 TAAGCTTCCTTATTATAACCCAGG 43

RESULT 7
CB210991/c
LOCUS      OML01271 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',
DEFINITION 41 bp mRNA linear EST 05-FEB-2003
ACCESSION  CB210991
VERSION     CB210991.1 GI:28257082
KEYWORDS    EST.
SOURCE      Oryza minuta
ORGANISM    Oryza minuta
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
              1 (bases 1 to 41)
              Shin, J.S.
              Oryza minuta HybridZAP-2.1 XR library
              Unpublished (2003)
              Contact: Jeong Sheop Shin
              Plant Molecular Genetics
              Graduate School of Biotechnology, University of Korea
              136-701 Anan-dong 5/1 Seoul, Korea
              Tel: 00 82 2 3290 3430
              Fax: 00 82 2 927 9028
              Email: jsshin@kucn.korea.ac.kr.
              Location/Qualifiers
FEATURES             source
     .
     /organism="Oryza minuta"
     /mol_type="mRNA"
     /db_xref="taxon:63629"
     /dev_stage="4-weeks after germination"
     /clone_lib="Oryza minuta HybridZAP-2.1 XR library"

```

```

Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Putative full length read
vector to vector length is 74
Seq primer: -40RP from Gibco.
Location/Qualifiers
1..73
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl057-4011"
/tissue_type="Degenerating cotyledons, 2 week old seedling"
/lab_host="DH10B"
/clone_lib="Gm-cl057"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 2 week old seedlings from
PI468916. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion.
The cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."

ORIGIN
Query Match      53.1%; Score 15.4; DB 12; Length 73;
Best Local Similarity 44.0%; Pred. No. 1.5e+05;
Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY  1 UAUGAUUCUUUUUGUAGCCCUAGG 25
    :|:::|:::|:::|:::|:::|
Db   19 TAAGCTTCCTTATTATAACCCAGG 43

RESULT 7
CB210991/c
LOCUS      OML01271 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',
DEFINITION 41 bp mRNA linear EST 05-FEB-2003
ACCESSION  CB210991
VERSION     CB210991.1 GI:28257082
KEYWORDS    EST.
SOURCE      Oryza minuta
ORGANISM    Oryza minuta
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
              1 (bases 1 to 41)
              Shin, J.S.
              Oryza minuta HybridZAP-2.1 XR library
              Unpublished (2003)
              Contact: Jeong Sheop Shin
              Plant Molecular Genetics
              Graduate School of Biotechnology, University of Korea
              136-701 Anan-dong 5/1 Seoul, Korea
              Tel: 00 82 2 3290 3430
              Fax: 00 82 2 927 9028
              Email: jsshin@kucn.korea.ac.kr.
              Location/Qualifiers
FEATURES             source
     .
     /organism="Oryza minuta"
     /mol_type="mRNA"
     /db_xref="taxon:63629"
     /dev_stage="4-weeks after germination"
     /clone_lib="Oryza minuta HybridZAP-2.1 XR library"

```


Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0277 row: P column: 20

Seq Primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 25.

FEATURES

source

1. .25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0277P20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 14.8; DB 28; Length 25;
Best Local Similarity 72.2%; Pred. No. 2.9e+05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 11 UUUGUAGCCUAGGGGC 28

Db 21 TTTCAGCCAGGGGC 4

RESULT 11

BE871815 60 bp mRNA linear EST 20-OCT-2000
LOCUS 601447803F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851880 5', mRNA sequence.

DEFINITION

BE871815

ACCESSION

BE871815

VERSION

BE871815.1 GI:10320591

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM9573 row: e column: 01

High quality sequence stop: 60.

Location/Qualifiers

source

1. .60

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="INAGE:3851880"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_65"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.8 kb. Library constructed by Life

Technologies."

ORIGIN

Query Match

Best Local Similarity

Matches

7; Conservative

9; Mismatches

2; Indels

0; Gaps

0;

Qy

2 AUGAUUUUUUUUAGC 19

Db

10 AGGATTTTCTTACG 27

RESULT 12

LOCUS

EX003595/c

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-373C10-017165,

Genomic survey sequence.

ACCESSION

EX003595

VERSION

EX003595.1 GI:26188555

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.

and Weisshaar,B.

A pipeline for automated high-throughput generation of FSTs

(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines

Unpublished

JOURNAL

REFERENCE

AUTHORS

Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.

Direct Submission

TITLE

Submitted (04-DEC-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

JOURNAL

COMMENT

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion close to or within gene At1g33610. The

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 60)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM9573 row: e column: 01

High quality sequence stop: 60.

Location/Qualifiers

source

1. .60

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="INAGE:3851880"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_65"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.8 kb. Library constructed by Life

Technologies."

ORIGIN

Query Match

Best Local Similarity

Matches

7; Conservative

9; Mismatches

2; Indels

0; Gaps

0;

Qy

2 AUGAUUUUUUUUAGC 19

Db

10 AGGATTTTCTTACG 27

RESULT 12

LOCUS

EX003595/c

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-373C10-017165,

Genomic survey sequence.

ACCESSION

EX003595

VERSION

EX003595.1 GI:26188555

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.

and Weisshaar,B.

A pipeline for automated high-throughput generation of FSTs

(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines

Unpublished

JOURNAL

REFERENCE

AUTHORS

Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.

Direct Submission

TITLE

Submitted (04-DEC-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

JOURNAL

COMMENT

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion close to or within gene At1g33610. The


```

Db      8 TTTTTCCTTTTCTGGGCGCTAGG 33

RESULT 15
BZ763921/c
LOCUS   72 bp  DNA  linear  GSS 13-MAR-2003
DEFINITION
SALK_122786.15.90.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_122786.15.90.n, genomic
survey sequence.
ACCESSION
BZ763921
VERSION  BZ763921.1  GI:28936474
KEYWORDS
SOURCE
ORGANISM  Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1. (bases 1 to 72)
REFERENCE
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
CONTACT: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1..72
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/clone="SALK_122786.15.90.n"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html
ORIGIN
Query Match 51.0%; Score 14.8; DB 28; Length 72;
Best Local Similarity 34.6%; Pred. No. 2.4e+05;
Matches 9; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 UAGUACUUUUUUGUAGCCUAGG 26
:||||: ::::: |||:|
55 TCTGATGTTTATATGTTCTAGG 30

RESULT 16
TA185E01P/c
LOCUS   72 bp  DNA  linear  GSS 13-DEC-2000
DEFINITION
T. brucei sheared genomic DNA clone 185e01, forward sequence,
genomic survey sequence.
ACCESSION
AL474065
VERSION  AL474065.1  GI:11840836
KEYWORDS
SOURCE
ORGANISM  Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1. (bases 1 to 72)
REFERENCE
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T\_brucei/.
FEATURES
Location/Qualifiers
1..72
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="185e01"
ORIGIN
Query Match 51.0%; Score 14.8; DB 29; Length 72;
Best Local Similarity 61.1%; Pred. No. 2.4e+05;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 12 UUGUAGCCCUAGGGGCU 29
:||||: |||||:|
66 TTCTAAGCCATAGGGGCT 49

RESULT 17
AZ775013/c
LOCUS   73 bp  DNA  linear  GSS 16-FEB-2001
DEFINITION
2M0004K20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0004K20 R, genomic survey sequence.
ACCESSION
AZ775013
VERSION  AZ775013.1  GI:12901065
KEYWORDS
SOURCE
ORGANISM  Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1. (bases 1 to 73)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rielly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: K column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 73.
Location/Qualifiers
1..73
/organism="Mus musculus"
FEATURES
source

```

```

/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004K20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PW042nv; Purified genomic DNA from M. musculus CS7BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

```

Query Match      51.0%; Score 14.8; DB 28; Length 73;
Best Local Similarity 61.1%; Pred. NO. 2.4e+05;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 11 UUUGUAAGCCCUAGGGGC 28
      ::||| |||||
Db 18 TTGTGTAATACCTAGGGGC 1

```

```
/clone_lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; vector: pcwv-sport6; Site:1:
Sal1; Site:2: Not1; Cloned unidirectionally. Primer:
Clono dr. Average insert size 1.25 kb. Life Technologies
catalog # : 11547-015"
```

ORIGIN

Query Match	51.0%	Score 14.8;	DB 9;	Length 74;
Best Local Similarity	38.9%	Prod. No. 2.4e+05;		
Matches	7;	Conservative	9;	Mismatches 2;
			Indels	0;
			Gaps	0;

ORIGIN

```

Query Match      51.0%; Score 14.8; DB 9; Length 76;
Best Local Similarity 38.9%; Pred. No. 2.4e+05;
Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY      2 AUGAUUUUUUUUGUAAGC 19
        ||||| : : : : : |||||
        ||||| : : : : : |||||
Db      49 ATGATTATTTTCTAAGC 32

```

FEATURES	SOURCE
1. The first part of the document is a letter from the author to the reader, explaining the purpose of the study and the methods used.	
2. The second part of the document is a review of the literature, discussing the current state of research on the topic.	
3. The third part of the document is a description of the experimental design, including the subjects, materials, and procedures.	
4. The fourth part of the document is a presentation of the results, including tables and figures.	
5. The fifth part of the document is a discussion of the results, comparing them to previous research and drawing conclusions.	
6. The sixth part of the document is a conclusion, summarizing the findings and suggesting future research.	
7. The seventh part of the document is a bibliography, listing all the sources cited in the paper.	
8. The eighth part of the document is an appendix, containing additional information related to the study.	
9. The ninth part of the document is a glossary, defining key terms used in the paper.	
10. The tenth part of the document is an index, providing a quick reference to specific sections of the paper.	

```

i...74
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:2410238"
/tissue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"

```

BI963697
LOCUS
DEFINITION ie63a09.x1 Melton Normalized Human Islet 4 N4-HIS 1 linear 76 bp mRNA EST 12-MAR-2002
CDNA clone IMAGE:5671576 3', mRNA sequence.

ACCESSION BI963697
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kastner, K., Leshka, L., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wyllie, J., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvilli, R., Williams, T., Jackson, Y., and Bowers, Y.

TITLE Endocrine Pancreas Consortium
JOURNAL
COMMENT Endocrine Pancreas Consortium
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov.

FEATURES

Location/Qualifiers
1..76
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5671576"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site: 1; Site 2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

ORIGIN

Query Match 51.0%; Score 14.8; DB 12; Length 76;
Best Local Similarity 30.8%; Pred. No. 2.4e+05;
Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 UAUAUUCUUUUUAAGCCUAGGG 26
: : : : :
Db 7 TTTTITTTTTTTCTTGCCCTAGGG 32

RESULT 21

AZ657549
LOCUS
DEFINITION 1M0533L18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

76 bp

DNA

linear

GSS 14-DEC-2000

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Location/Qualifiers
1..76
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0533L18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114|9p|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 14.8; DB 28; Length 76;
Best Local Similarity 38.5%; Pred. No. 2.4e+05;
Matches 10; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUAAGCCUAGGGCU 29
: : : : :
Db 44 GTTTCCTTTTGAGGCACACAGCT 69

RESULT 22

CG549254
LOCUS
DEFINITION OST152329 Mus musculus 129Sv/Ev Mus musculus genomic clone

77 bp

DNA

linear

GSS 01-OCT-2003

clone UUGC1M0533L18 R, genomic survey sequence.

AZ657549

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0533 row: L column: 18

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 76.

OST152329, genomic survey sequence.
 CG549254
 CG549254.1 GI:37335841
 GSS.
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 77)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggett,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,W.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.F.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..77
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129SV/Ev"
 /db_xref="taxon:10090"
 /clone="OST152329"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129SV/Ev"

Query Match 51.0%; Score 14.8; DB 29; Length 77;
 Best Local Similarity 44.4%; Pred. No. 2.4e+05;
 Matches 8; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGUAGC 19
 |:::|||||
 6 AGGATCTTTTCTAAGC 23

RESULT 23
 BX287070
 LOCUS BX287070 49 bp DNA linear GSS 07-MAR-2003
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-396F11-018295,
 genomic survey sequence.
 ACCESSION BX287070
 VERSION BX287070.1 GI:28886066
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Siedler,H.
 and Weisshaar,B.
 A pipeline for automated high-throughput generation of FSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 Unpublished
 JOURNAL
 REFERENCE
 2
 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 TITLE for flanking sequence tag based reverse genetics
 JOURNAL
 REFERENCE
 3 (bases 1 to 49)

Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
 Direct Submission
 Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone MZ24. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/
 Location/Qualifiers
 1..49
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-396F11-018295"
 /notes="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

Query Match 50.3%; Score 14.6; DB 29; Length 49;
 Best Local Similarity 41.4%; Pred. No. 3.1e+05;
 Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 UAUGAUCUUUUUGUAGCCUAGGGGCU 29
 :||:|||||
 8 TAAGCTTAATGTGTAAAGGCTATGGAT 36

RESULT 24
 BG236504
 LOCUS BG236504 52 bp mRNA linear EST 12-FEB-2001
 DEFINITION nai44c06.x1 NCI_CGAP_HN20 Homo sapiens cDNA clone IMAGE:4262795 3',
 mRNA sequence.
 ACCESSION BG236504
 VERSION BG236504.1 GI:12750351
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 52)
 NCI/NIH-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
 National Cancer Institute / National Institute of Dental Research,
 Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1..52
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4262795"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_HN20"

/note="Organ: normal head/neck tissue; Vector: pAMP1; mRNA made from head/neck tissue, cDNA made by oligo-dT priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA Library Preparation: David B. Krizman, Ph.D."

ORIGIN

Query Match 50.3%; Score 14.6; DB 12; Length 52;
Best Local Similarity 38.1%; Pred. No. 3.1e+05;
Matches 8; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
QY 6 UUUUUUUUAGGCCUAGGG 26
DB 1 TTTTITTTTAAAGTCTAGGG 21

RESULT 25

BH911891/c

LOCUS

DEFINITION Arabidopsis thaliana genomic clone SALK_072729.50.65.x, genomic survey sequence.

ACCESSION

BH911891

VERSION

BH911891.1

SOURCE

GSS

ORGANISM

Arabidopsis thaliana (thale cress)

REFERENCE

1 (bases 1 to 62)

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadzinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J., and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 5' end of

At4g13720.

Class: TDNA tagged.

Location/Qualifiers

1..62

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_072729.50.65.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

1 UAUUUUUUUUAGGCCUAGGG 29

46 TATAATTTTTTACTAGGCGCTAGACCT 18

RESULT 26

CG563472/c

LOCUS

DEFINITION

ACCESSION

CG563472

VERSION

CG563472.1

SOURCE

GSS

ORGANISM

Mus musculus (house mouse)

REFERENCE

1 (bases 1 to 63)

AUTHORS

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

Piggott,J., Beltrandeirio,H., Buxton,E.C., Edwards,J., Finch,R.A.,

Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,

Key,B.W. Jr., Kipp,P., Kohlhaufl,B., Ma,Z.-Q., Markesich,D.,

Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,

Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1..63

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="129SV/EV"

/db_xref="taxon:10090"

/clone="OST186777"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129SV/EV"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

4 GAUUCUUUUUAGGCCUAG 24

45 GTTCTCTGTGTAAGCCCTGG 25

RESULT 27

AI139668/c

LOCUS

DEFINITION

ACCESSION

AI139668

VERSION

AI139668.1

SOURCE

GSS

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 64)

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

Tumor Gene Index

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.lml.nih.gov) for further information.

/lab host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 50.3%; Score 14.6; DB 28; Length 66;
 Best Local Similarity 52.4%; Pred. No. 3e+05;
 Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 8 CUUUUUAAGCCCUAGGGCC 28

DB 18 CTTCTGTACACCCCTAGGGCC 38

RESULT 30

BI865610/c

LOCUS

DEFINITION

ft22h02.y1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5082459

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 73)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Persson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R., and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Other ESTs: ft22h02.x1

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@wustl.edu

CDNA Library constructed by S. Lin DNA Sequencing by: Washington

University Genome Sequencing Center Clone distribution: the

I.M.A.G.E. Consortium/LINL, send email to: info@image.linl.gov

Seq primer: T3 ET from Amersham.

Location/Qualifiers

1..73

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:5082459"

/sex="mixed"

/dev_stage="adult"

FEATURES

source

/lab host="DH10B (phage-resistant)"
 /clone lib="Zebrafish neuronal"
 /note="Organ: brain; Vector: pBluescript (modified);
 Site 1: DraIII(V); Site 2: DraIII(X); Library is cloned
 directionally between the DraIII(X) and DraIII(V) sites
 and has been amplified. Library constructed by S. Lin."

ORIGIN

Query Match 50.3%; Score 14.6; DB 12; Length 73;
 Best Local Similarity 27.6%; Pred. No. 2.9e+05;
 Matches 8; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 UUAUAUUUUUUUAAGCCCUAGGGCCU 29

DB 59 TTTTTTTTTTTTTTGAGCTCTTCGGGCT 31

RESULT 31

EX001193

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-104G08-018339,

genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

REFERENCE

AUTHORS

Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Siedler, H.

and Weisshaar, B.

A pipeline for automated high-throughput generation of ESTs

(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines

Unpublished

2

Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.

A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

for flanking sequence tag based reverse genetics

Unpublished

3 (bases 1 to 73)

Rosso, M., Strizhov, N., Li, Y. and Weisshaar, B.

Direct Submission

Submitted (04-DEC-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion within the locus defined by clone T22B15.

The sequences are generated at the MPI for Plant Breeding Research

in the context of the GABI-Kat project. GABI-Kat is part of the

German Plant Genomics program designated 'GABI'. Information on

line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1..73

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-104G08-018339"

/clone lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector pAC161. The lines contain one or more T-DNA

insertions. The DNA fragment(s) resulting from the PCR

were directly sequenced to determine the genomic sequence

flanking the insertion. Sequences displaying significant

similarity to the A. thaliana nuclear genome sequence were

processed for submission. T-DNA derived sequences were

removed"

ORIGIN

source

1. .43
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0410K10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PWD42rv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.7%; Score 14.4; DB 28; Length 43;
 Best Local Similarity 58.3%; Pred. No. 3.8e+05;
 Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 AUUCUUUUGAAGCCUAGGGGC 28
 | : : : : :
 DB 43 ATACAGTTTGACGACCAAGGGGC 20

RESULT 35

AL771575
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-181D09-013603,
 DEFINITION genomic survey sequence.
 ACCESSION AL771575.1 GI:215333777
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE

1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Siedler,H.
 and Weisshaar,B.
 A pipeline for automated high-throughput generation of PSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines

AUTHORS

2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics

JOURNAL

REFERENCE Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 TITLE This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone F12G12.
 The sequences are generated at the MPI for Plant Breeding Research
 in the context of the GABI-Kat project. GABI-Kat is part of the

JOURNAL

REFERENCE Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
 TITLE Direct Submission

JOURNAL

COMMENT Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone F12G12.
 The sequences are generated at the MPI for Plant Breeding Research
 in the context of the GABI-Kat project. GABI-Kat is part of the

FEATURES

source

1. .44
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-181D09-013603"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA from
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

ORIGIN

Query Match 49.7%; Score 14.4; DB 29; Length 44;
 Best Local Similarity 45.8%; Pred. No. 3.8e+05;
 Matches 11; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 6 UUCUUUUGAAGCCUAGGGGC 29
 | : : : : :
 DB 17 TGCCTTTTGAGGCCCTATGGGAT 40

RESULT 36

BI865449
 LOCUS 54 bp mRNA linear EST 11-OCT-2001
 DEFINITION ft22h02.x1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5082459
 3' mRNA sequence.

ACCESSION

BI865449
 VERSION BI865449.1 GI:16059582

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS

1 (bases 1 to 54)
 Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
 Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
 Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 WashU Zebrafish EST Project 1998
 Unpublished (1998)

TITLE

JOURNAL

COMMENT

Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: zbrfish@wustl.edu

CDNA Library constructed by S. Lin DNA sequencing by: Washington
 University Genome Sequencing Center Clone distribution: the
 I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: T7 from Gibco.

FEATURES

source

1. .54
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:5082459"
 /sex="mixed"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Zebrafish neuronal"

German Plant Genomics program designated 'GABI'. Information on
 line availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. .44

```

/note=Organ: brain; Vector: pBluescript (modified);
Site 1: DralII(Y); Site 2: DralIII(X); Library is cloned
directionally between the DraIII(X) and DraiI(Y) sites
and has been amplified. Library constructed by S. Lin. "

ORIGIN
Query Match          49.7%; Score 14.4; DB 12; Length 54;
Best Local Similarity 33.3%; Pred.No. 3.6e+05;
Matches      8; Conservative 10; Mismatches   6; Indels    0; Gaps    0;

QY      6 UUUUUUUGUAAGCCUAGGGGU 29
       : ::::: : ||| : ||| :
Db       5 TTTTITTTTGAGCTCTTCGGGCT 28

RESULT 37
AL595218
LOCUS      AL595218
DEFINITION XGC-gastrula Silurana tropicalis cDNA clone TGas002h22 5';
mRNA sequence.
ACCESSION AL595218
VERSION   AL595218.1 GI:15007293
KEYWORDS EST.
SOURCE    Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 60)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Huckle E
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TGas002h22.pkKSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from sug of poly A+ RNA from stages 10-13
gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.

FEATURES             Location/Qualifiers
     1..60
         /organism="Silurana tropicalis"
         /mol_type="mRNA"
         /db_xref="taxon:8364"
         /clone="TGas002h22"
         /dev_stage="gastrula (stages 10.5-12 mixed)"
         /lab_hosts="Escherichia coli XL1-blue"
         /clone_lib="XGC-gastrula"
         /note=Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN
Query Match          49.7%; Score 14.4; DB 9; Length 60;
Best Local Similarity 37.5%; Pred.No. 3.6e+05;
Matches      9; Conservative 9; Mismatches   6; Indels    0; Gaps    0;

QY      2 AUGAUCUUUUUGUAAGCCCUAGG 25
       : ||| : : : | : ||| :
bb      8 ATGATTTTTATTGTTTCTGAG 31

```

BG362434 63 bp mRNA linear EST 08-MAR-2001
 gb72b09.y1 Moss EST library PPG Physcomitrella patens cDNA clone
 PEP SOURCE_ID: 5', mRNA sequence.
 BG362434
 BG362434.1 GI:13251531
 EST
 Physcomitrella patens
 Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 63)
 Quatrano, R., Bashardes, S., Cove, D., Cuning, A., Knight, C.,
 Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
 Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Stepcoe, M., Gibbons, M., Harvey, N., Ritter, E.,
 Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
 Leeds/Wash U Moss EST Project
 Unpublished (1999)
 Contact: Ralph Quatrano
 Leeds/Wash U Moss EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..63
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
 /db_xref="taxon:3218"
 /clone="PEP SOURCE ID:"
 /tissue_type="gametophore: 30 day old tissue,
 ammonium-grown"
 /lab_host="DH10B"
 /clone_lib="Moss EST library PBQ"
 /note="Vector: PAMPI1; Construction of the cDNA library was
 performed by Dr. W. Gregg Clark using a modification of
 the cDNA synthesis protocol developed in the laboratory of
 Dr. Michael Lovett by Dr. Yulia Korshunova (personal
 communication). First polyA + RNA was isolated from total
 gametophore RNA using oligo dt magnetic beads. Following
 this, first strand cDNA synthesis was performed on the
 bead-bound polyA + RNA, during which an oligonucleotide
 anchor sequence was incorporated onto the 5'-ends of the
 cDNA. PCR amplification was then used to synthesize the
 second strand, to amplify the double stranded DNA, and to
 incorporate dUTP containing sequences into the ends of the
 double stranded cDNA. This DNA was size selected and
 cloned into PAMPI1 using the CloneAMP PAMPI System (Life
 Technologies, GibcoBRL) for cloning amplification products
 by a non-restriction site dependent process. The cloning
 was directional based on sequence asymmetry introduced at
 the ends during PCR amplification. The 3' cDNA ends are in
 the proximal to the NotI site of the multiple cloning site in
 PAMPI1. This annealing mixture was transformed into
 chemically competent DH10B cells and selected for
 ampicillin resistant growth. The resulting clones (about
 330,000) were pooled to make the library."

RESULT 38
BG362434/c

QY	1	UAUGAUCUUUUUGUAAGCCCUAG	24
	:	:	:
	:	:	:
	:	:	:
	:	:	:
DB	42	TTTTTTTTTTTTTGAACCCCAAG	19

RESULT 39
CG664319/c
LOCUS
DEFINITION
OS7451176 Mus musculus 129Sv/Ev Mus musculus genomic clone
OS7451176, genomic survey sequence.
ACCESSION
CG664319
VERSION
CG664319.1 GI:37489168
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 65)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

source
1..65
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/ev"
/db_xref="taxon:10090"
/clone="OST451176"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/ev"

ORIGIN

Query Match 49.7%; Score 14.4; DB 29; Length 65;
Best Local Similarity 33.3%; Pred. No. 3.5e+05;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 6 UUCUUUUUUAAGCCCUAGGGGCU 29
Db 63 TTTTGTAGATCTCTGGGTT 40

RESULT 40
AI584052/c
LOCUS
DEFINITION
AI584052 67 bp mRNA linear EST 14-DEC-1999
ts13b02.x1 NCI CGAP Panel Homo sapiens cDNA clone IMAGE:2228427 3',
similar to TR.000599 000599 CON1; contains element MER22
repetitive element 1, mRNA sequence.
ACCESSION
AI584052
VERSION
AI584052.1 GI:4569949
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 67)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1154 Std Error: 0.00
Seq Primer: 40UP from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES

source
Location/Qualifiers
1..67
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2228427"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Panel"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN

Query Match 49.7%; Score 14.4; DB 9; Length 67;
Best Local Similarity 37.5%; Pred. No. 3.5e+05;
Matches 9; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUCUUUUUAAGCCCUAGGGG 27
Db 38 GGTTCCTTTTTCCTAGGGG 15

Search completed: April 18, 2004, 09:59:04
Job time: 1568.67 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:34:53 ; Search time 36.6667 Seconds
(without alignments)
438.916 Million cell updates/sec

Title: US-09-310-844C-25

Perfect score: 29

Sequence: 1 aaagaucuuuuuuaagcccaagggcu 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 915622

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
C 1	15.2	52.4	33	Sequence 5, Appl
C 2	15.2	52.4	47	Sequence 1097, Ap
C 3	15.2	52.4	75	Sequence 6, Appl
C 4	14.8	51.0	29	Sequence 25, Appl
C 5	14.8	51.0	29	Sequence 25, Appl
C 6	14.8	51.0	29	Sequence 25, Appl
C 7	14.8	51.0	29	Sequence 25, Appl
C 8	14.8	51.0	29	Sequence 25, Appl
C 9	14.8	51.0	29	Sequence 25, Appl
C 10	14.8	51.0	29	Sequence 25, Appl
C 11	14.8	51.0	29	Sequence 25, Appl
C 12	14.8	51.0	29	Sequence 25, Appl
C 13	14.6	50.3	32	Sequence 18, Appl
C 14	14.6	50.3	32	Sequence 18, Appl
C 15	14.2	49.0	25	Sequence 18, Appl
C 16	14.2	49.0	25	Sequence 18, Appl
C 17	14.2	49.0	25	Sequence 18, Appl
C 18	14.2	49.0	25	Sequence 18, Appl
C 19	14.2	49.0	25	Sequence 18, Appl
C 20	14.2	49.0	25	Sequence 18, Appl
C 21	14.2	49.0	25	Sequence 18, Appl
C 22	14.2	49.0	25	Sequence 18, Appl
C 23	14.2	49.0	25	Sequence 18, Appl
C 24	14.2	49.0	25	Sequence 18, Appl
C 25	14.2	49.0	25	Sequence 18, Appl
C 26	14.2	49.0	25	Sequence 18, Appl
C 27	14.2	49.0	25	Sequence 18, Appl

C 28	13.8	47.6	25	3	US-08-943-731-336	Sequence 336, App
C 29	13.8	47.6	33	4	US-09-199-542B-76	Sequence 76, Appl
C 30	13.8	47.6	47	4	US-09-671-317-663	Sequence 663, App
C 31	13.8	47.6	50	4	US-09-428-082B-401	Sequence 401, App
C 32	13.8	47.6	57	4	US-09-428-082B-414	Sequence 414, App
C 33	13.8	47.6	60	4	US-09-428-082B-415	Sequence 415, App
C 34	13.8	47.6	61	4	US-09-428-082B-400	Sequence 400, App
C 35	13.6	46.9	41	4	US-09-565-156A-2	Sequence 2, Appl
C 36	13.6	46.9	47	4	US-09-423-978-1843	Sequence 1843, Ap
C 37	13.6	46.9	47	4	US-09-402-266B-10	Sequence 10, Appl
C 38	13.6	46.9	52	4	US-09-310-463-6	Sequence 6, Appl
C 39	13.6	46.9	52	4	US-08-842-248A-6	Sequence 6, Appl
C 40	13.6	46.9	79	1	US-08-472-255A-136	Sequence 136, App
C 41	13.6	46.9	79	1	US-08-472-255A-136	Sequence 136, App
C 42	13.6	46.9	79	3	US-08-472-255B-136	Sequence 136, App
C 43	13.6	46.9	79	3	US-08-952-793-136	Sequence 136, App
C 44	13.6	46.9	79	4	US-09-849-928-136	Sequence 136, App
C 45	13.6	46.9	79	5	PCT-US96-09455A-136	Sequence 136, App
C 46	13.4	46.2	32	3	US-08-718-738-16	Sequence 16, Appl
C 47	13.4	46.2	32	3	US-09-221-844-16	Sequence 16, Appl
C 48	13.4	46.2	32	5	PCT-US95-03323A-16	Sequence 16, Appl
C 49	13.4	46.2	40	4	US-09-428-082B-418	Sequence 418, App
C 50	13.4	46.2	46	1	US-08-171-389-42	Sequence 42, Appl
C 51	13.4	46.2	46	1	US-08-171-389-45	Sequence 45, Appl
C 52	13.4	46.2	46	1	US-08-123-936-42	Sequence 42, Appl
C 53	13.4	46.2	46	1	US-08-123-936-45	Sequence 45, Appl
C 54	13.4	46.2	46	2	US-08-475-228A-45	Sequence 45, Appl
C 55	13.4	46.2	46	2	US-08-475-228A-45	Sequence 45, Appl
C 56	13.4	46.2	46	3	US-08-482-080A-42	Sequence 42, Appl
C 57	13.4	46.2	46	3	US-08-482-080A-45	Sequence 45, Appl
C 58	13.4	46.2	46	4	US-09-354-947-42	Sequence 42, Appl
C 59	13.4	46.2	46	4	US-09-354-947-45	Sequence 45, Appl
C 60	13.4	46.2	46	5	PCT-US93-12388-42	Sequence 42, Appl
C 61	13.4	46.2	46	5	PCT-US93-12388-45	Sequence 45, Appl
C 62	13.4	46.2	50	1	US-08-245-754A-13	Sequence 13, Appl
C 63	13.4	46.2	50	1	US-08-171-389-46	Sequence 46, Appl
C 64	13.4	46.2	50	1	US-08-123-936-46	Sequence 46, Appl
C 65	13.4	46.2	50	2	US-08-475-228A-46	Sequence 46, Appl
C 66	13.4	46.2	50	2	US-08-597-731-13	Sequence 13, Appl
C 67	13.4	46.2	50	3	US-08-482-080A-46	Sequence 46, Appl
C 68	13.4	46.2	50	4	US-09-354-947-46	Sequence 46, Appl
C 69	13.4	46.2	50	5	PCT-US93-12388-46	Sequence 46, Appl
C 70	13.2	45.5	22	3	US-08-969-317-9	Sequence 9, Appl
C 71	13.2	45.5	25	4	US-08-827-988-1097	Sequence 1097, Ap
C 72	13.2	45.5	25	4	US-08-827-988-1105	Sequence 1105, Ap
C 73	13.2	45.5	27	1	US-08-485-602-23	Sequence 23, Appl
C 74	13.2	45.5	27	1	US-08-757-180-22	Sequence 22, Appl
C 75	13.2	45.5	27	1	US-08-745-638-23	Sequence 23, Appl
C 76	13.2	45.5	29	4	US-09-304-232-120	Sequence 120, App
C 77	13.2	45.5	29	4	US-09-304-232-120	Sequence 120, App
C 78	13.2	45.5	32	4	US-09-031-889A-12	Sequence 12, Appl
C 79	13.2	45.5	38	1	US-08-372-224A-1480	Sequence 1480, Ap
C 80	13.2	45.5	38	1	US-08-435-628-1480	Sequence 1480, Ap
C 81	13.2	45.5	38	2	US-08-292-620A-2069	Sequence 2069, Ap
C 82	13.2	45.5	38	3	US-09-071-845-2069	Sequence 2069, Ap
C 83	13.2	45.5	47	4	US-08-422-978-1851	Sequence 1851, Ap
C 84	13.2	45.5	64	1	US-08-271-364A-2	Sequence 2, Appl
C 85	13.2	45.5	66	4	US-08-956-171B-2731	Sequence 2731, Ap
C 86	13.2	45.5	69	4	US-09-732-210-25	Sequence 25, Appl
C 87	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 88	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 89	13.2	45.5	69	4	US-08-846-762-43	Sequence 43, Appl
C 90	13.2	45.5	69	4	US-07-598-737C-6	Sequence 6, Appl
C 91	13.2	45.5	69	4	US-08-084-718-19	Sequence 19, Appl
C 92	13.2	45.5	69	4	US-08-443-976-19	Sequence 19, Appl
C 93	13.2	45.5	69	4	US-08-443-977-19	Sequence 19, Appl
C 94	13.2	45.5	69	4	US-09-641-638-833	Sequence 833, App
C 95	13.2	45.5	69	4	US-09-622-978-2842	Sequence 2842, Ap
C 96	13.2	45.5	69	4	US-08-316-293-42	Sequence 42, Appl
C 97	13.2	45.5	69	4	US-07-875-758-7	Sequence 7, Appl
C 98	13.2	45.5	69	4	US-09-011-336-63	Sequence 63, Appl
C 99	13.2	45.5	69	4	US-08-488-402A-157	Sequence 157, App
C 100	13.2	45.5	69	4	US-08-484-552A-157	Sequence 157, App

101	13	44.8	70	5	PCT-US96-09472-157	Sequence 157, Appl	174	12.6	43.4	45	1	US-08-171-389-342	Sequence 342, Appl
102	13	44.8	78	1	US-08-400-256-11	Sequence 11, Appl	175	12.6	43.4	45	1	US-08-123-936-130	Sequence 130, Appl
103	13	44.8	78	3	US-08-975-365-11	Sequence 11, Appl	176	12.6	43.4	45	1	US-08-123-936-342	Sequence 342, Appl
104	12.8	44.1	18	4	US-09-422-978-5466	Sequence 5466, Ap	177	12.6	43.4	45	2	US-08-475-228A-130	Sequence 130, Appl
105	12.8	44.1	20	2	US-09-289-368-95	Sequence 85, Appl	178	12.6	43.4	45	2	US-08-475-228A-342	Sequence 342, Appl
106	12.8	44.1	20	4	US-09-323-357-18	Sequence 18, Appl	179	12.6	43.4	45	2	US-08-482-080A-130	Sequence 130, Appl
107	12.8	44.1	24	4	US-09-015-160-75	Sequence 75, Appl	180	12.6	43.4	45	3	US-08-482-080A-342	Sequence 342, Appl
108	12.8	44.1	28	4	US-08-646-861-28	Sequence 28, Appl	181	12.6	43.4	45	3	US-08-290-995-4	Sequence 4, Appl
109	12.8	44.1	30	3	US-08-621-841-51	Sequence 51, Appl	182	12.6	43.4	45	4	US-09-354-947-130	Sequence 130, Appl
110	12.8	44.1	33	1	US-08-181-271A-96	Sequence 96, Appl	183	12.6	43.4	45	4	US-09-354-947-342	Sequence 342, Appl
111	12.8	44.1	33	1	US-08-449-315-96	Sequence 96, Appl	184	12.6	43.4	45	5	PCT-US93-12388-130	Sequence 130, Appl
112	12.8	44.1	33	1	US-08-444-803-96	Sequence 96, Appl	185	12.6	43.4	45	5	PCT-US93-12388-342	Sequence 342, Appl
113	12.8	44.1	33	1	US-08-094-534-20	Sequence 20, Appl	186	12.6	43.4	48	4	US-09-238-356-64	Sequence 64, Appl
114	12.8	44.1	33	1	US-08-449-043-96	Sequence 96, Appl	187	12.6	43.4	49	4	US-08-961-888-6	Sequence 7, Appl
115	12.8	44.1	33	1	US-08-456-265A-96	Sequence 96, Appl	188	12.6	43.4	49	4	US-08-961-888-7	Sequence 7, Appl
116	12.8	44.1	33	1	US-08-456-416-96	Sequence 96, Appl	189	12.6	43.4	50	1	US-08-171-389-343	Sequence 343, Appl
117	12.8	44.1	33	1	US-08-455-244-96	Sequence 96, Appl	190	12.6	43.4	50	1	US-08-123-936-343	Sequence 343, Appl
118	12.8	44.1	33	1	US-08-454-876-96	Sequence 96, Appl	191	12.6	43.4	50	2	US-08-475-228A-343	Sequence 343, Appl
119	12.8	44.1	33	2	US-08-457-364-96	Sequence 96, Appl	192	12.6	43.4	50	3	US-08-482-080A-343	Sequence 31, Appl
120	12.8	44.1	33	2	US-08-456-262-96	Sequence 96, Appl	193	12.6	43.4	50	3	US-09-390-867A-31	Sequence 31, Appl
121	12.8	44.1	33	2	US-08-456-240-96	Sequence 96, Appl	194	12.6	43.4	50	4	US-09-354-947-343	Sequence 31, Appl
122	12.8	44.1	33	2	US-08-455-736-96	Sequence 96, Appl	195	12.6	43.4	50	4	US-09-354-947-343	Sequence 31, Appl
123	12.8	44.1	33	2	US-08-971-217-96	Sequence 96, Appl	196	12.6	43.4	50	5	PCT-US93-12388-343	Sequence 343, Appl
124	12.8	44.1	33	2	US-08-581-543-20	Sequence 20, Appl	197	12.6	43.4	51	4	US-09-425-585-6	Sequence 6, Appl
125	12.8	44.1	33	3	US-09-350-600-96	Sequence 96, Appl	198	12.6	43.4	51	4	US-09-953-321-6	Sequence 6, Appl
126	12.8	44.1	33	4	US-09-906-234-96	Sequence 96, Appl	199	12.6	43.4	51	4	US-09-479-645A-188	Sequence 188, Appl
127	12.8	44.1	33	4	PCT-US94-08000-20	Sequence 20, Appl	200	12.6	43.4	52	2	US-08-464-073-22	Sequence 22, Appl
128	12.8	44.1	35	4	US-10-045-428A-16	Sequence 16, Appl	201	12.6	43.4	62	2	US-08-428-258-22	Sequence 22, Appl
129	12.8	44.1	36	1	US-08-319-492B-332	Sequence 332, Appl	202	12.6	43.4	62	3	US-08-937-610-16	Sequence 16, Appl
130	12.8	44.1	40	2	US-08-425-684-58	Sequence 58, Appl	203	12.6	43.4	62	3	US-08-416-516A-22	Sequence 22, Appl
131	12.8	44.1	40	2	US-08-675-503-58	Sequence 58, Appl	204	12.6	43.4	66	4	US-09-268-347-50	Sequence 50, Appl
132	12.8	44.1	40	4	US-09-245-803-58	Sequence 58, Appl	205	12.6	43.4	66	4	US-08-940-136-261	Sequence 261, Appl
133	12.8	44.1	43	3	US-09-306-998-16	Sequence 16, Appl	206	12.6	43.4	67	3	US-09-275-850-315	Sequence 315, Appl
134	12.8	44.1	47	4	US-09-422-978-2381	Sequence 2381, Ap	207	12.6	43.4	69	2	US-08-790-963-100	Sequence 100, Appl
135	12.8	44.1	48	2	US-08-477-553A-16	Sequence 16, Appl	208	12.6	43.4	69	3	US-09-371-774-100	Sequence 100, Appl
136	12.8	44.1	54	3	US-08-369-822C-30	Sequence 30, Appl	209	12.6	43.4	71	3	US-09-275-850-94	Sequence 94, Appl
137	12.8	44.1	54	3	US-08-582-776C-45	Sequence 45, Appl	210	12.6	43.4	71	3	US-09-275-850-95	Sequence 95, Appl
138	12.8	44.1	54	3	US-08-434-831B-42	Sequence 42, Appl	211	12.6	43.4	72	2	US-08-464-073-20	Sequence 20, Appl
139	12.8	44.1	54	4	US-09-315-926A-27	Sequence 27, Appl	212	12.6	43.4	72	2	US-08-428-252-20	Sequence 20, Appl
140	12.8	44.1	61	1	US-08-702-795-3	Sequence 3, Appl	213	12.6	43.4	72	3	US-08-416-516A-20	Sequence 20, Appl
141	12.8	44.1	69	3	US-08-483-511-77	Sequence 77, Appl	214	12.6	43.4	77	1	US-08-442-572-1	Sequence 1, Appl
142	12.8	44.1	71	1	US-08-131-365B-39	Sequence 39, Appl	215	12.6	43.4	77	1	US-08-361-795-1	Sequence 1, Appl
143	12.8	44.1	71	2	US-08-668-123-39	Sequence 39, Appl	216	12.6	43.4	77	5	PCT-US95-05600-84	Sequence 84, Appl
144	12.6	43.4	19	1	US-08-384-490-3	Sequence 3, Appl	217	12.6	43.4	78	3	US-08-945-737-77	Sequence 77, Appl
145	12.6	43.4	19	1	US-08-459-383-3	Sequence 3, Appl	218	12.6	43.4	78	3	US-09-258-797-77	Sequence 77, Appl
146	12.6	43.4	23	4	US-09-470-661A-22	Sequence 22, Appl	219	12.4	42.8	22	4	US-09-445-283C-45	Sequence 5, Appl
147	12.6	43.4	25	3	US-08-692-787-76	Sequence 76, Appl	220	12.4	42.8	23	3	US-09-033-055A-5	Sequence 5, Appl
148	12.6	43.4	25	3	US-09-304-232-781	Sequence 781, Appl	221	12.4	42.8	28	2	US-08-726-090-9	Sequence 9, Appl
149	12.6	43.4	29	4	US-08-894-808-8	Sequence 8, Appl	222	12.4	42.8	28	4	US-09-911-983-1	Sequence 1, Appl
150	12.6	43.4	35	1	US-08-041-538-3	Sequence 3, Appl	223	12.4	42.8	30	1	US-08-324-243-30	Sequence 30, Appl
151	12.6	43.4	35	1	US-08-463-642-3	Sequence 3, Appl	224	12.4	42.8	30	1	US-08-532-390-30	Sequence 30, Appl
152	12.6	43.4	35	1	US-08-465-602-3	Sequence 3, Appl	225	12.4	42.8	30	3	US-08-717-294-30	Sequence 30, Appl
153	12.6	43.4	35	2	US-08-465-157-3	Sequence 3, Appl	226	12.4	42.8	30	5	PCT-US95-11511-30	Sequence 30, Appl
154	12.6	43.4	35	2	PCT-US91-09422-3	Sequence 3, Appl	227	12.4	42.8	31	3	US-09-033-055A-7	Sequence 7, Appl
155	12.6	43.4	35	5	5281520-10	Patent No. 5281520	228	12.4	42.8	33	4	US-09-622-540A-10	Sequence 10, Appl
156	12.6	43.4	36	2	US-08-882-083-7	Sequence 7, Appl	229	12.4	42.8	33	4	US-09-622-540A-10	Sequence 10, Appl
157	12.6	43.4	36	2	US-08-558-107-7	Sequence 7, Appl	230	12.4	42.8	34	4	US-09-581-070-2	Sequence 2, Appl
158	12.6	43.4	36	2	US-09-243-539-7	Sequence 7, Appl	231	12.4	42.8	34	4	US-09-581-070-5	Sequence 5, Appl
159	12.6	43.4	36	3	US-08-218-369-7	Sequence 7, Appl	232	12.4	42.8	37	1	US-08-049-264C-55	Sequence 55, Appl
160	12.6	43.4	36	4	US-08-218-369-15	Sequence 15, Appl	233	12.4	42.8	37	1	US-08-476-562-55	Sequence 55, Appl
161	12.6	43.4	36	4	US-08-218-369-15	Sequence 15, Appl	234	12.4	42.8	37	1	US-08-479-723A-55	Sequence 55, Appl
162	12.6	43.4	36	4	PCT-US95-03745-7	Sequence 7, Appl	235	12.4	42.8	37	5	PCT-US94-04310-55	Sequence 54, Appl
163	12.6	43.4	36	5	PCT-US95-03745-7	Sequence 7, Appl	236	12.4	42.8	38	4	US-09-371-772B-8446	Sequence 54, Appl
164	12.6	43.4	36	5	PCT-US95-03745-7	Sequence 7, Appl	237	12.4	42.8	38	4	US-08-049-264C-54	Sequence 54, Appl
165	12.6	43.4	36	5	PCT-US95-03745-7	Sequence 7, Appl	238	12.4	42.8	44	1	US-08-476-562-54	Sequence 54, Appl
166	12.6	43.4	42	3	US-09-136-411-10	Sequence 10, Appl	239	12.4	42.8	44	1	US-08-479-723A-54	Sequence 54, Appl
167	12.6	43.4	42	6	5281520-11	Patent No. 5281520	240	12.4	42.8	44	5	PCT-US94-04310-54	Sequence 54, Appl
168	12.6	43.4	43	1	US-08-041-538-4	Sequence 4, Appl	241	12.4	42.8	47	4	US-09-422-978-639	Sequence 3759, Ap
169	12.6	43.4	43	1	US-08-463-642-4	Sequence 4, Appl	242	12.4	42.8	47	4	US-09-422-978-3759	Sequence 37, Appl
170	12.6	43.4	43	1	US-08-455-602-4	Sequence 4, Appl	243	12.4	42.8	48	4	US-03-623-326-37	Sequence 858, Appl
171	12.6	43.4	43	2	US-08-455-602-4	Sequence 4, Appl	244	12.4	42.8	51	4	US-09-443-199C-868	Sequence 4, Appl
172	12.6	43.4	43	5	PCT-US91-09422-4	Sequence 4, Appl	245	12.4	42.8	65	4	US-09-352-540A-4	Sequence 4, Appl
173	12.6	43.4	45	1	US-08-171-389-130	Sequence 130, Appl	246	12.4	42.8	65	4	US-09-759-645-4	Sequence 4, Appl

247	12.4	42.8	65	4	US-10-002-528-4	Sequence 4, Appli	Sequence 4, Appli	12.2	42.1	51	2	US-08-471-025-16	Sequence 16, Appl
248	12.4	42.8	68	4	US-08-356-171B-2762	Sequence 2762, Ap	Sequence 2762, Ap	12.2	42.1	51	3	US-08-473-446-39	Sequence 39, Appl
249	12.4	42.1	17	1	US-08-373-124A-1795	Sequence 1795, Ap	Sequence 1795, Ap	12.2	42.1	51	3	US-08-460-736-16	Sequence 16, Appl
250	12.2	42.1	17	1	US-08-435-628-1795	Sequence 1795, Ap	Sequence 1795, Ap	12.2	42.1	51	4	US-09-354-138-16	Sequence 16, Appl
251	12.2	42.1	17	4	US-09-827-998-281	Sequence 281, App	Sequence 281, App	12.2	42.1	51	4	US-09-535-370-16	Sequence 16, Appl
252	12.2	42.1	17	4	US-09-827-998-282	Sequence 282, App	Sequence 282, App	12.2	42.1	51	4	US-09-136-159A-16	Sequence 16, Appl
253	12.2	42.1	17	4	US-09-827-998-283	Sequence 283, App	Sequence 283, App	12.2	42.1	51	5	PCT-US96-00547-16	Sequence 16, Appl
254	12.2	42.1	19	3	US-08-832-896-53	Sequence 53, Appl	Sequence 53, Appl	12.2	42.1	51	6	5514566-10	Patent No. 5514566
255	12.2	42.1	20	4	US-09-198-452A-6382	Sequence 6382, Ap	Sequence 6382, Ap	12.2	42.1	54	4	US-09-315-326A-23	Sequence 23, Appl
256	12.2	42.1	20	4	US-09-601-144-11	Sequence 11, Appl	Sequence 11, Appl	12.2	42.1	55	3	US-08-434-099A-17	Sequence 17, Appl
257	12.2	42.1	22	4	US-09-375-673B-42	Sequence 42, Appl	Sequence 42, Appl	12.2	42.1	58	4	US-09-621-976-12180	Sequence 12180, A
258	12.2	42.1	23	3	US-08-817-913-25	Sequence 25, Appl	Sequence 25, Appl	12.2	42.1	59	1	US-08-009-265-3	Sequence 3, Appli
259	12.2	42.1	25	4	US-09-687-637B-4	Sequence 4, Appli	Sequence 4, Appli	12.2	42.1	59	3	US-08-483-511-35	Sequence 35, Appl
260	12.2	42.1	25	4	US-09-827-998-1086	Sequence 1086, Ap	Sequence 1086, Ap	12.2	42.1	59	5	PCT-US93-01009-35	Sequence 35, Appl
261	12.2	42.1	25	4	US-09-827-998-1106	Sequence 1106, Ap	Sequence 1106, Ap	12.2	42.1	70	2	US-08-488-402A-127	Sequence 127, App
262	12.2	42.1	29	1	US-08-467-420A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	70	2	US-08-484-522A-127	Sequence 127, App
263	12.2	42.1	29	1	US-08-470-110A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	70	5	PCT-US96-09472-127	Sequence 127, App
264	12.2	42.1	29	1	US-08-667-769A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	78	1	US-08-351-748-19	Sequence 19, Appl
265	12.2	42.1	29	1	US-08-940-371-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	78	1	US-08-430-536A-19	Sequence 19, Appl
266	12.2	42.1	29	2	US-08-483-636-30	Sequence 30, Appl	Sequence 30, Appl	12.2	42.1	78	2	US-08-684-547-19	Sequence 19, Appl
267	12.2	42.1	29	2	US-08-483-632-30	Sequence 30, Appl	Sequence 30, Appl	12.2	42.1	78	4	US-09-621-976-12398	Sequence 12398, A
268	12.2	42.1	29	3	US-08-637-647-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	78	5	PCT-US93-02246-19	Sequence 19, Appl
269	12.2	42.1	29	4	US-08-793-273C-19	Sequence 19, Appl	Sequence 19, Appl	12.2	42.1	80	1	US-07-832-905B-61	Sequence 61, Appl
270	12.2	42.1	29	4	US-09-304-232-323	Sequence 323, App	Sequence 323, App	12.2	42.1	80	1	US-07-832-905B-62	Sequence 62, Appl
271	12.2	42.1	29	5	PCT-US94-07659-13	Sequence 13, App	Sequence 13, App	12.2	42.1	80	2	US-08-700-757-61	Sequence 61, Appl
272	12.2	42.1	29	5	PCT-US95-11684-19	Sequence 19, Appl	Sequence 19, Appl	12.2	42.1	80	2	US-08-700-757-62	Sequence 62, Appl
273	12.2	42.1	29	5	PCT-US95-1708A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	80	2	US-08-860-882A-43	Sequence 43, Appl
274	12.2	42.1	30	1	US-08-479-487-43	Sequence 43, Appl	Sequence 43, Appl	12.2	42.1	80	4	US-09-011-769A-10	Sequence 10, Appl
275	12.2	42.1	30	1	US-08-479-487-55	Sequence 55, Appl	Sequence 55, Appl	12.2	42.1	80	4	US-09-166-186-198	Sequence 198, App
276	12.2	42.1	30	3	US-08-854-170-3	Sequence 3, Appli	Sequence 3, Appli	12.2	42.1	80	3	US-09-333-932-198	Sequence 198, App
277	12.2	42.1	30	3	US-08-913-842-47	Sequence 47, Appl	Sequence 47, Appl	12.2	42.1	21	3	US-09-333-932-198	Sequence 12, Appl
278	12.2	42.1	30	4	US-09-898-627-2	Sequence 2, Appli	Sequence 2, Appli	12.2	42.1	21	4	US-09-422-978-6777	Sequence 6777, Ap
279	12.2	42.1	32	3	US-09-295-028-77	Sequence 77, Appl	Sequence 77, Appl	12.2	42.1	22	4	US-09-375-673B-49	Sequence 49, Appl
280	12.2	42.1	32	3	US-09-692-064-8	Sequence 8, Appli	Sequence 8, Appli	12.2	42.1	22	4	US-09-375-673B-51	Sequence 51, Appl
281	12.2	42.1	32	4	US-09-693-542-77	Sequence 77, Appl	Sequence 77, Appl	12.2	42.1	22	4	US-07-714-687-54	Sequence 54, Appl
282	12.2	42.1	32	4	US-09-693-542-77	Sequence 77, Appl	Sequence 77, Appl	12.2	42.1	22	4	US-08-224-391-55	Sequence 54, Appl
283	12.2	42.1	33	3	US-07-861-458C-59	Sequence 59, Appl	Sequence 59, Appl	12.2	42.1	33	1	US-08-484-304-54	Sequence 54, Appl
284	12.2	42.1	34	6	5519127-14	Patent No. 5519127	Patent No. 5519127	12.2	42.1	34	2	US-08-484-304-54	Sequence 104, App
285	12.2	42.1	36	1	US-07-756-251A-6	Sequence 6, Appli	Sequence 6, Appli	12.2	42.1	35	1	US-08-102-567-17	Sequence 17, Appl
286	12.2	42.1	36	1	US-08-696-566-7	Sequence 7, Appli	Sequence 7, Appli	12.2	42.1	35	3	US-08-462-947-17	Sequence 17, Appl
287	12.2	42.1	36	3	US-08-911-860-7	Sequence 7, Appli	Sequence 7, Appli	12.2	42.1	35	3	US-07-714-687-55	Sequence 55, Appl
288	12.2	42.1	38	1	US-08-373-124A-303	Sequence 303, App	Sequence 303, App	12.2	42.1	37	1	US-08-224-391-55	Sequence 55, Appl
289	12.2	42.1	38	1	US-08-373-124A-809	Sequence 809, App	Sequence 809, App	12.2	42.1	37	1	US-08-484-304-55	Sequence 55, Appl
290	12.2	42.1	38	1	US-08-373-124A-877	Sequence 877, App	Sequence 877, App	12.2	42.1	37	1	US-09-306-290-16	Sequence 16, Appl
291	12.2	42.1	38	1	US-08-373-124A-1328	Sequence 1328, Ap	Sequence 1328, Ap	12.2	42.1	40	3	US-09-306-290-16	Sequence 146, App
292	12.2	42.1	38	1	US-08-435-628-303	Sequence 303, App	Sequence 303, App	12.2	42.1	41	4	US-08-280-116-146	Sequence 146, App
293	12.2	42.1	38	1	US-08-435-628-809	Sequence 809, App	Sequence 809, App	12.2	42.1	47	1	US-08-464-083-3	Sequence 3, Appli
294	12.2	42.1	38	1	US-08-435-628-877	Sequence 877, App	Sequence 877, App	12.2	42.1	47	1	US-08-443-965B-5	Sequence 5, Appli
295	12.2	42.1	38	1	US-08-435-628-1328	Sequence 1328, Ap	Sequence 1328, Ap	12.2	42.1	47	2	US-08-425-989B-5	Sequence 5, Appli
296	12.2	42.1	39	6	5519127-34	Patent No. 5519127	Patent No. 5519127	12.2	42.1	47	2	US-08-443-966B-5	Sequence 5, Appli
297	12.2	42.1	40	4	US-09-294-584A-4	Sequence 4, Appli	Sequence 4, Appli	12.2	42.1	47	3	US-08-469-587A-3	Sequence 3, Appli
298	12.2	42.1	41	2	US-08-833-814A-6	Sequence 6, Appli	Sequence 6, Appli	12.2	42.1	47	3	US-08-318-038D-3	Sequence 3, Appli
299	12.2	42.1	42	3	US-08-434-099A-16	Sequence 16, Appl	Sequence 16, Appl	12.2	42.1	47	3	US-08-227-496C-3	Sequence 3, Appli
300	12.2	42.1	44	1	US-07-832-905B-58	Sequence 58, Appl	Sequence 58, Appl	12.2	42.1	47	4	US-09-671-317-703	Sequence 703, App
301	12.2	42.1	44	2	US-08-700-757-58	Sequence 58, Appl	Sequence 58, Appl	12.2	42.1	47	4	US-09-422-978-3352	Sequence 3352, Ap
302	12.2	42.1	45	2	US-08-860-882A-19	Sequence 19, Appl	Sequence 19, Appl	12.2	42.1	55	4	US-08-956-171E-1690	Sequence 1690, Ap
303	12.2	42.1	45	3	US-08-997-918-10	Sequence 10, Appl	Sequence 10, Appl	12.2	42.1	55	4	US-08-956-171E-5024	Sequence 5024, Ap
304	12.2	42.1	45	3	US-08-997-918-24	Sequence 24, Appl	Sequence 24, Appl	12.2	42.1	58	3	US-08-275-850-263	Sequence 263, App
305	12.2	42.1	45	4	US-09-011-769A-15	Sequence 15, Appl	Sequence 15, Appl	12.2	42.1	58	3	US-08-258-287B-31	Sequence 31, Appl
306	12.2	42.1	47	4	US-09-641-638-1000	Sequence 1000, Ap	Sequence 1000, Ap	12.2	42.1	59	3	US-08-368-704C-31	Sequence 31, Appl
307	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	61	1	US-08-197-782-26	Sequence 26, Appl
308	12.2	42.1	47	4	US-09-671-317-692	Sequence 692, App	Sequence 692, App	12.2	42.1	61	1	US-08-459-850-26	Sequence 26, Appl
309	12.2	42.1	47	4	US-09-422-978-2286	Sequence 2286, Ap	Sequence 2286, Ap	12.2	42.1	61	1	US-08-459-214-26	Sequence 26, Appl
310	12.2	42.1	47	4	US-08-282-147-43	Sequence 43, Appl	Sequence 43, Appl	12.2	42.1	61	4	US-09-313-221A-80	Sequence 80, Appl
311	12.2	42.1	50	3	US-08-220-151-39	Sequence 39, Appl	Sequence 39, Appl	12.2	42.1	61	4	US-09-543-848B-66	Sequence 66, Appl
312	12.2	42.1	51	1	US-08-413-118-39	Sequence 39, Appl	Sequence 39, Appl	12.2	42.1	66	4	US-09-858-994-10	Sequence 10, Appl
313	12.2	42.1	51	1	US-08-224-657-16	Sequence 16, Appl	Sequence 16, Appl	12.2	42.1	66	4	US-09-858-994-10	Sequence 11, Appl
314	12.2	42.1	51	1	US-08-257-073-83	Sequence 83, Appl	Sequence 83, Appl	12.2	42.1	69	4	US-09-134-600C-20	Sequence 20, Appl
315	12.2	42.1	51	2	US-08-184-009-16	Sequence 16, Appl	Sequence 16, Appl	12.2	42.1	78	4	US-09-858-994-5	Sequence 5, Appli
316	12.2	42.1	51	2	US-08-486-969-16	Sequence 16, Appl	Sequence 16, Appl	12.2	42.1	78	4	US-09-401-064-324	Sequence 324, App
317	12.2	42.1	51	2	US-08-417-210A-16	Sequence 16, Appl	Sequence 16, Appl	12.2	42.1	80	1	US-08-208-886C-21	Sequence 21, Appl
318	12.2	42.1	51	2	US-08-458-356-16	Sequence 16, Appl	Sequence 16, Appl	12.2	42.1	80	1	US-08-704-744-21	Sequence 21, Appl
319	12.2	42.1	51	2				12.2	42.1	80	1		

393	12	41.4	80	1	US-08-469-557-21	Sequence 21, Appl	C 466	11.8	40.7	47	4	US-09-641-638-852	Sequence 852, App
394	12	41.4	80	2	US-08-290-793B-21	Sequence 21, Appl	C 467	11.8	40.7	47	4	US-09-671-317-839	Sequence 829, App
395	11.8	40.7	80	3	US-09-827-998-284	Sequence 284, App	C 468	11.8	40.7	47	4	US-09-422-978-787	Sequence 734, App
396	11.8	40.7	17	4	US-09-827-998-285	Sequence 285, App	C 469	11.8	40.7	47	4	US-09-422-978-2486	Sequence 2486, App
397	11.8	40.7	20	4	US-09-827-998-285	Sequence 285, App	C 470	11.8	40.7	47	4	US-09-422-978-2486	Sequence 2486, App
398	11.8	40.7	17	4	US-09-827-998-285	Sequence 285, App	C 471	11.8	40.7	47	4	US-09-892-188B-12	Sequence 12, Appl
399	11.8	40.7	24	2	US-08-451-822A-11	Sequence 11, Appl	C 472	11.8	40.7	54	1	US-08-073-963-3	Sequence 3, Appl
400	11.8	40.7	24	2	US-08-323-430-11	Sequence 11, Appl	C 473	11.8	40.7	54	1	US-08-073-963-4	Sequence 4, Appl
401	11.8	40.7	25	4	US-09-827-998-1107	Sequence 1107, App	C 474	11.8	40.7	54	1	US-08-487-412-3	Sequence 3, Appl
402	11.8	40.7	25	4	US-09-827-998-1108	Sequence 1108, App	C 475	11.8	40.7	54	1	US-08-487-412-4	Sequence 4, Appl
403	11.8	40.7	26	1	US-08-599-252-43	Sequence 43, Appl	C 476	11.8	40.7	54	2	US-08-418-848A-57	Sequence 57, Appl
404	11.8	40.7	26	5	PCT-US96-06352-43	Sequence 43, Appl	C 477	11.8	40.7	54	4	US-08-584-040-2949	Sequence 2949, App
405	11.8	40.7	26	5	PCT-US96-06583-43	Sequence 43, Appl	C 478	11.8	40.7	54	4	US-08-706-945D-105	Sequence 105, App
406	11.8	40.7	27	6	5258283-10	Patent No. 5258283	C 479	11.8	40.7	54	4	US-09-371-772B-8615	Sequence 8615, App
407	11.8	40.7	29	1	US-08-531-556-99	Sequence 99, Appl	C 480	11.8	40.7	54	6	5459046-8	Patent No. 5459046
408	11.8	40.7	29	2	US-08-690-73A-30	Sequence 30, Appl	C 481	11.8	40.7	57	4	US-09-318-786-7	Sequence 7, Appl
409	11.8	40.7	29	3	US-08-742-185-30	Sequence 30, Appl	C 482	11.8	40.7	60	3	US-08-478-097A-32	Sequence 32, Appl
410	11.8	40.7	30	1	US-08-381-280-24	Sequence 24, Appl	C 483	11.8	40.7	60	3	US-09-496-398-32	Sequence 32, Appl
411	11.8	40.7	30	2	US-08-445-533-24	Sequence 24, Appl	C 484	11.8	40.7	61	3	US-08-952-793-362	Sequence 362, App
412	11.8	40.7	30	3	US-09-052-085-24	Sequence 24, Appl	C 485	11.8	40.7	61	4	US-09-849-928-362	Sequence 362, App
413	11.8	40.7	31	4	US-09-063-733A-20	Sequence 20, Appl	C 486	11.8	40.7	61	5	PCT-US96-09455A-362	Sequence 362, App
414	11.8	40.7	32	1	US-09-429-693-3	Sequence 3, Appl	C 487	11.8	40.7	62	1	US-08-206-384-7	Sequence 7, Appl
415	11.8	40.7	32	2	US-08-867-941-60	Sequence 60, Appl	C 488	11.8	40.7	62	3	US-08-752-722-7	Sequence 7, Appl
416	11.8	40.7	32	3	US-09-074-658-60	Sequence 60, Appl	C 489	11.8	40.7	63	3	US-09-337-712-68	Sequence 68, Appl
417	11.8	40.7	32	4	US-09-230-288-13	Sequence 13, Appl	C 490	11.8	40.7	64	4	US-09-059-625-17	Sequence 17, Appl
418	11.8	40.7	34	3	US-08-544-381B-174	Sequence 174, App	C 491	11.8	40.7	66	3	US-09-337-712-64	Sequence 64, Appl
419	11.8	40.7	36	1	US-08-319-492B-234	Sequence 234, App	C 492	11.8	40.7	68	4	US-09-193-612B-13	Sequence 13, Appl
420	11.8	40.7	36	1	US-08-319-492B-581	Sequence 581, App	C 493	11.8	40.7	70	4	US-09-647-036A-6	Sequence 6, Appl
421	11.8	40.7	36	1	US-08-363-240A-924	Sequence 924, App	C 494	11.8	40.7	72	3	US-08-950-961-23	Sequence 23, Appl
422	11.8	40.7	36	2	US-08-292-620A-918	Sequence 918, App	C 495	11.8	40.7	72	4	US-09-479-776-23	Sequence 23, Appl
423	11.8	40.7	36	2	US-08-585-684B-327	Sequence 327, App	C 496	11.8	40.0	20	4	US-09-488-856A-29	Sequence 29, Appl
424	11.8	40.7	36	2	US-08-585-684B-2044	Sequence 2044, App	C 497	11.6	40.0	20	4	US-09-689-255C-18	Sequence 18, Appl
425	11.8	40.7	36	2	US-08-585-684B-2385	Sequence 2385, App	C 498	11.6	40.0	21	4	US-09-422-978-10520	Sequence 10520, A
426	11.8	40.7	36	3	US-09-071-845-918	Sequence 918, App	C 499	11.6	40.0	21	4	US-08-507-634-6	Sequence 6, Appl
427	11.8	40.7	36	3	US-09-440-001-3	Sequence 3, Appl	C 500	11.6	40.0	24	2	US-09-327-229-25	Sequence 25, Appl
428	11.8	40.7	36	3	US-09-038-073-327	Sequence 327, App	C 501	11.6	40.0	24	5	PCT-US95-12608-25	Sequence 25, Appl
429	11.8	40.7	36	3	US-09-038-073-2044	Sequence 2044, App	C 502	11.6	40.0	25	3	US-08-891-789B-32	Sequence 32, Appl
430	11.8	40.7	36	3	US-09-038-073-2385	Sequence 2385, App	C 503	11.6	40.0	25	3	US-09-601-258-7	Sequence 7, Appl
431	11.8	40.7	36	3	US-09-038-073-2386	Sequence 2386, App	C 504	11.6	40.0	26	1	US-08-154-019-5	Sequence 5, Appl
432	11.8	40.7	36	3	US-08-793-634B-18	Sequence 18, Appl	C 505	11.6	40.0	26	1	US-08-461-333-5	Sequence 5, Appl
433	11.8	40.7	36	4	US-09-374-963-19	Sequence 19, Appl	C 506	11.6	40.0	26	1	US-08-461-333-12	Sequence 12, Appl
434	11.8	40.7	36	4	US-09-605-685-3	Sequence 3, Appl	C 507	11.6	40.0	26	3	US-08-464-167-5	Sequence 5, Appl
435	11.8	40.7	37	4	US-08-705-477E-59	Sequence 59, Appl	C 508	11.6	40.0	26	3	US-08-464-167-12	Sequence 12, Appl
436	11.8	40.7	38	1	US-08-373-124A-577	Sequence 545, App	C 509	11.6	40.0	26	3	US-09-158-313-5	Sequence 5, Appl
437	11.8	40.7	38	1	US-08-373-124A-577	Sequence 577, App	C 510	11.6	40.0	26	3	US-09-158-313-12	Sequence 12, Appl
438	11.8	40.7	38	1	US-08-373-124A-1199	Sequence 1199, App	C 511	11.6	40.0	26	3	US-08-476-798-5	Sequence 5, Appl
439	11.8	40.7	38	1	US-08-373-124A-1306	Sequence 1306, App	C 512	11.6	40.0	26	3	US-08-476-798-12	Sequence 12, Appl
440	11.8	40.7	38	1	US-08-373-124A-1584	Sequence 1584, App	C 513	11.6	40.0	26	4	US-09-689-255C-6	Sequence 6, Appl
441	11.8	40.7	38	1	US-08-373-124A-2326	Sequence 2326, App	C 514	11.6	40.0	28	4	US-09-438-954-21	Sequence 21, Appl
442	11.8	40.7	38	1	US-08-373-124A-2432	Sequence 2432, App	C 515	11.6	40.0	29	4	US-09-304-232-345	Sequence 345, App
443	11.8	40.7	38	1	US-08-373-124A-2508	Sequence 2508, App	C 516	11.6	40.0	29	4	US-09-937-832-21	Sequence 21, Appl
444	11.8	40.7	38	1	US-08-373-124A-2584	Sequence 2584, App	C 517	11.6	40.0	30	4	US-09-374-963-19	Sequence 19, Appl
445	11.8	40.7	38	1	US-08-435-628-545	Sequence 545, App	C 518	11.6	40.0	31	2	US-08-347-563A-35	Sequence 35, Appl
446	11.8	40.7	38	1	US-08-435-628-577	Sequence 577, App	C 519	11.6	40.0	31	3	US-08-485-942A-35	Sequence 35, Appl
447	11.8	40.7	38	1	US-08-435-628-1199	Sequence 1199, App	C 520	11.6	40.0	31	3	US-08-488-209A-35	Sequence 35, Appl
448	11.8	40.7	38	1	US-08-435-628-1306	Sequence 1306, App	C 521	11.6	40.0	31	3	US-08-483-211A-35	Sequence 35, Appl
449	11.8	40.7	38	1	US-08-435-628-1594	Sequence 1594, App	C 522	11.6	40.0	31	4	US-08-488-223A-35	Sequence 35, Appl
450	11.8	40.7	38	1	US-08-435-628-2326	Sequence 2326, App	C 523	11.6	40.0	31	4	US-08-488-223A-35	Sequence 35, Appl
451	11.8	40.7	38	1	US-08-435-628-2432	Sequence 2432, App	C 524	11.6	40.0	31	4	US-08-488-223A-35	Sequence 35, Appl
452	11.8	40.7	38	1	US-08-435-628-2508	Sequence 2508, App	C 525	11.6	40.0	31	4	US-08-488-223A-35	Sequence 35, Appl
453	11.8	40.7	38	1	US-08-435-628-2584	Sequence 2584, App	C 526	11.6	40.0	32	2	US-08-959-998-407	Sequence 407, App
454	11.8	40.7	38	4	US-09-325-554-10	Sequence 10, Appl	C 527	11.6	40.0	32	4	US-09-225-528-407	Sequence 407, App
455	11.8	40.7	38	4	US-09-325-554-11	Sequence 11, Appl	C 528	11.6	40.0	32	4	US-09-225-528-407	Sequence 407, App
456	11.8	40.7	38	4	US-09-371-772B-7942	Sequence 7942, App	C 529	11.6	40.0	32	4	US-08-979-847B-104	Sequence 104, App
457	11.8	40.7	38	4	US-08-679-645-24	Sequence 645, App	C 530	11.6	40.0	34	4	US-09-063-733A-52	Sequence 52, Appl
458	11.8	40.7	42	4	US-08-980-832-65	Sequence 65, Appl	C 531	11.6	40.0	34	4	US-08-488-446-612	Sequence 612, App
459	11.8	40.7	43	3	US-09-422-978-3434	Sequence 3434, App	C 532	11.6	40.0	34	4	US-08-467-344A-612	Sequence 612, App
460	11.8	40.7	43	4	US-09-820-923B-65	Sequence 65, Appl	C 533	11.6	40.0	35	6	542260-12	Patent No. 542260
461	11.8	40.7	44	2	US-08-343-443B-39	Sequence 39, Appl	C 534	11.6	40.0	36	4	US-09-746-359A-42	Sequence 42, Appl
462	11.8	40.7	44	2	US-07-832-905B-59	Sequence 59, Appl	C 535	11.6	40.0	36	4	US-09-593-580B-29	Sequence 29, Appl
463	11.8	40.7	47	1	US-07-832-905B-59	Sequence 59, Appl	C 536	11.6	40.0	37	1	US-07-598-737C-5	Sequence 5, Appl
464	11.8	40.7	47	2	US-07-832-905B-59	Sequence 59, Appl	C 537	11.6	40.0	37	1	US-08-084-718-18	Sequence 18, Appl
465	11.8	40.7	47	4	US-09-641-638-663	Sequence 663, App	C 538	11.6	40.0	37	1		

539	11.6	40.0	37	1	US-08-443-976-18	Sequence 18, Appl	c 612	11.6	40.0	66	4	US-08-956-171B-1643	Sequence 1643, Ap
540	11.6	40.0	37	1	US-08-443-977-18	Sequence 18, Appl	c 613	11.6	40.0	69	3	US-08-832-985-14	Sequence 14, Appl
541	11.6	40.0	37	1	US-08-721-458B-59	Sequence 59, Appl	c 614	11.6	40.0	69	4	US-09-410-903-95	Sequence 95, Appl
542	11.6	40.0	38	1	US-08-390-850-840	Sequence 840, Appl	c 615	11.6	40.0	69	4	US-08-835-159-14	Sequence 14, Appl
543	11.6	40.0	38	1	US-08-390-850-862	Sequence 862, Appl	c 616	11.6	40.0	69	4	US-09-621-976-16527	Sequence 16527, A
544	11.6	40.0	38	1	US-08-390-850-897	Sequence 897, Appl	c 617	11.6	40.0	70	3	US-09-364-380-11	Sequence 11, Appl
545	11.6	40.0	38	1	US-08-373-124A-453	Sequence 453, Appl	c 618	11.6	40.0	71	3	US-09-275-850-143	Sequence 143, App
546	11.6	40.0	38	1	US-08-373-124A-591	Sequence 591, Appl	c 619	11.6	40.0	75	3	US-08-952-457-6	Sequence 6, Appli
547	11.6	40.0	38	1	US-08-373-124A-1426	Sequence 1426, Ap	c 620	11.6	40.0	75	4	US-09-025-769B-311	Sequence 311, App
548	11.6	40.0	38	1	US-08-373-124A-1500	Sequence 1500, Ap	c 621	11.6	40.0	76	1	US-07-593-657-10	Sequence 10, Appl
549	11.6	40.0	38	1	US-08-435-634-840	Sequence 840, App	c 622	11.6	40.0	76	4	US-09-025-769B-310	Sequence 310, App
550	11.6	40.0	38	1	US-08-435-634-862	Sequence 862, App	c 623	11.6	40.0	76	4	US-09-963-137-32	Sequence 32, Appl
551	11.6	40.0	38	1	US-08-435-634-897	Sequence 897, App	c 624	11.4	39.3	14	3	US-08-847-844A-99	Sequence 99, Appl
552	11.6	40.0	38	1	US-08-435-628-453	Sequence 453, App	c 625	11.4	39.3	17	4	US-08-584-040-3752	Sequence 3752, Ap
553	11.6	40.0	38	1	US-08-435-628-591	Sequence 591, App	c 626	11.4	39.3	17	4	US-08-371-772B-1519	Sequence 1519, Ap
554	11.6	40.0	38	1	US-08-435-628-1426	Sequence 1426, Ap	c 627	11.4	39.3	17	4	US-08-371-772B-1519	Sequence 1519, Ap
555	11.6	40.0	38	1	US-08-435-628-1500	Sequence 1500, Ap	c 628	11.4	39.3	21	2	US-08-117-952-169	Sequence 169, App
556	11.6	40.0	38	1	US-08-469-260A-623	Sequence 623, App	c 629	11.4	39.3	21	4	US-08-745-995A-37	Sequence 37, Appl
557	11.6	40.0	38	4	US-08-469-260A-623	Sequence 623, App	c 630	11.4	39.3	21	4	US-09-005-352-37	Sequence 37, Appl
558	11.6	40.0	38	4	US-08-488-446-611	Sequence 611, App	c 631	11.4	39.3	22	4	US-09-375-673B-52	Sequence 52, Appl
559	11.6	40.0	38	4	US-08-488-446-623	Sequence 623, App	c 632	11.4	39.3	24	3	US-09-253-025-53	Sequence 53, Appl
560	11.6	40.0	38	4	US-08-467-344A-611	Sequence 611, App	c 633	11.4	39.3	24	4	US-09-356-806-82	Sequence 82, Appl
561	11.6	40.0	38	4	US-08-467-344A-623	Sequence 623, App	c 634	11.4	39.3	24	4	US-09-356-806-82	Sequence 82, Appl
562	11.6	40.0	40	3	US-09-306-290-34	Sequence 34, Appl	c 635	11.4	39.3	25	1	US-07-842-089E-38	Sequence 38, Appl
563	11.6	40.0	41	1	US-07-931-473B-63	Sequence 63, Appl	c 636	11.4	39.3	25	1	US-08-264-485-38	Sequence 38, Appl
564	11.6	40.0	41	1	US-07-931-473B-87	Sequence 87, Appl	c 637	11.4	39.3	25	2	US-08-690-734A-54	Sequence 54, Appl
565	11.6	40.0	41	1	US-07-114-131C-63	Sequence 63, Appl	c 638	11.4	39.3	25	3	US-08-742-185-54	Sequence 54, Appl
566	11.6	40.0	41	1	US-07-114-131C-87	Sequence 87, Appl	c 639	11.4	39.3	25	4	US-09-027-287-22	Sequence 22, Appl
567	11.6	40.0	41	1	US-08-412-110-63	Sequence 63, Appl	c 640	11.4	39.3	25	4	US-09-252-656B-22	Sequence 22, Appl
568	11.6	40.0	41	1	US-08-412-110-87	Sequence 87, Appl	c 641	11.4	39.3	26	2	US-08-533-323-22	Sequence 22, Appl
569	11.6	40.0	41	1	US-08-409-442A-63	Sequence 63, Appl	c 642	11.4	39.3	26	2	US-08-533-323-22	Sequence 22, Appl
570	11.6	40.0	41	1	US-08-409-442A-87	Sequence 87, Appl	c 643	11.4	39.3	27	1	US-08-758-306-904	Sequence 904, App
571	11.6	40.0	41	1	US-08-409-442A-356	Sequence 356, App	c 644	11.4	39.3	27	4	US-08-584-040-6545	Sequence 6545, Ap
572	11.6	40.0	41	2	US-08-469-609A-63	Sequence 63, Appl	c 645	11.4	39.3	27	5	PCT-US93-09070-13	Sequence 13, Appl
573	11.6	40.0	41	2	US-08-469-609A-87	Sequence 87, Appl	c 646	11.4	39.3	28	1	US-08-220-606B-31	Sequence 31, Appl
574	11.6	40.0	41	2	US-08-469-609A-356	Sequence 356, App	c 647	11.4	39.3	29	1	US-08-220-606B-31	Sequence 31, Appl
575	11.6	40.0	41	3	US-09-143-190-63	Sequence 63, Appl	c 648	11.4	39.3	29	1	US-08-586-024-1	Sequence 1, Appl
576	11.6	40.0	41	3	US-09-143-190-87	Sequence 87, Appl	c 649	11.4	39.3	29	3	US-09-020-818-1	Sequence 1, Appl
577	11.6	40.0	41	3	US-09-143-190-356	Sequence 356, App	c 650	11.4	39.3	29	3	US-08-907-740-1	Sequence 1, Appl
578	11.6	40.0	41	3	US-09-502-344-63	Sequence 63, Appl	c 651	11.4	39.3	29	4	US-09-797-467-1	Sequence 1, Appl
579	11.6	40.0	41	4	US-09-502-344-87	Sequence 87, Appl	c 652	11.4	39.3	30	1	US-08-381-280-26	Sequence 26, Appl
580	11.6	40.0	41	4	US-09-502-344-356	Sequence 356, App	c 653	11.4	39.3	30	1	US-08-453-924-11	Sequence 11, Appl
581	11.6	40.0	41	4	US-09-551-656-55	Sequence 55, Appl	c 654	11.4	39.3	30	2	US-08-445-533-26	Sequence 26, Appl
582	11.6	40.0	41	4	US-09-650-855-55	Sequence 55, Appl	c 655	11.4	39.3	30	3	US-09-052-085-26	Sequence 26, Appl
583	11.6	40.0	43	4	US-09-434-354-4	Sequence 4, Appl	c 656	11.4	39.3	32	1	US-08-299-810A-17	Sequence 17, Appl
584	11.6	40.0	45	3	US-08-721-458B-62	Sequence 62, Appl	c 657	11.4	39.3	32	1	US-08-299-810A-18	Sequence 18, Appl
585	11.6	40.0	46	1	US-08-794-153-5	Sequence 5, Appl	c 658	11.4	39.3	32	1	US-08-299-810A-20	Sequence 20, Appl
586	11.6	40.0	46	1	US-09-115-566-5	Sequence 5, Appl	c 659	11.4	39.3	32	2	US-08-599-602-15	Sequence 15, Appl
587	11.6	40.0	46	3	US-09-478-189-125	Sequence 125, App	c 660	11.4	39.3	32	2	US-08-544-381B-173	Sequence 173, App
588	11.6	40.0	46	4	US-08-399-696-26	Sequence 26, App	c 661	11.4	39.3	32	3	US-09-197-816-15	Sequence 15, Appl
589	11.6	40.0	47	1	US-09-422-978-988	Sequence 988, App	c 662	11.4	39.3	32	3	US-08-387-805-3	Sequence 3, Appl
590	11.6	40.0	47	4	US-09-422-978-1021	Sequence 1021, Ap	c 663	11.4	39.3	33	4	US-09-075-019-12	Sequence 12, Appl
591	11.6	40.0	47	4	US-09-422-978-1076	Sequence 1076, Ap	c 664	11.4	39.3	34	3	US-08-470-535-18	Sequence 18, Appl
592	11.6	40.0	47	4	US-09-422-978-1093	Sequence 1093, Ap	c 665	11.4	39.3	36	3	US-08-250-802-8	Sequence 8, Appl
593	11.6	40.0	47	4	US-09-422-978-1513	Sequence 1513, Ap	c 666	11.4	39.3	36	3	US-08-469-260A-631	Sequence 631, App
594	11.6	40.0	47	4	US-09-422-978-1806	Sequence 1806, Ap	c 667	11.4	39.3	36	4	US-08-469-260A-631	Sequence 631, App
595	11.6	40.0	47	4	US-09-422-978-3054	Sequence 3054, Ap	c 668	11.4	39.3	36	4	US-08-469-260A-631	Sequence 631, App
596	11.6	40.0	47	4	US-09-422-978-3129	Sequence 3129, Ap	c 669	11.4	39.3	36	4	US-08-469-260A-631	Sequence 631, App
597	11.6	40.0	47	4	US-09-358-972-122	Sequence 122, App	c 670	11.4	39.3	36	4	US-09-643-217-8	Sequence 8, Appl
598	11.6	40.0	50	3	US-09-383-316-21	Sequence 21, Appl	c 671	11.4	39.3	37	1	US-08-741-881-106	Sequence 106, App
599	11.6	40.0	50	4	US-08-956-171B-1996	Sequence 1996, Ap	c 672	11.4	39.3	37	1	US-08-739-158-106	Sequence 106, App
600	11.6	40.0	51	4	US-09-443-199C-18	Sequence 18, Appl	c 673	11.4	39.3	37	2	US-08-739-167-106	Sequence 106, App
601	11.6	40.0	51	4	US-09-443-199C-854	Sequence 854, App	c 674	11.4	39.3	37	3	US-08-404-796-106	Sequence 106, App
602	11.6	40.0	51	4	US-09-275-850-287	Sequence 287, App	c 675	11.4	39.3	37	3	US-08-931-869-106	Sequence 106, App
603	11.6	40.0	53	3	US-09-619-213B-45	Sequence 45, Appl	c 676	11.4	39.3	37	3	US-09-350-399-106	Sequence 106, App
604	11.6	40.0	58	4	US-09-956-171B-5102	Sequence 5102, Ap	c 677	11.4	39.3	37	4	US-09-236-140A-106	Sequence 106, App
605	11.6	40.0	61	4	US-08-619-213B-45	Sequence 45, Appl	c 678	11.4	39.3	38	1	US-08-104-072B-34	Sequence 34, Appl
606	11.6	40.0	63	1	US-08-084-718-46	Sequence 46, Appl	c 679	11.4	39.3	38	4	US-09-371-772B-7874	Sequence 7874, Ap
607	11.6	40.0	63	1	US-08-443-976-46	Sequence 46, Appl	c 680	11.4	39.3	38	4	US-09-371-772B-8215	Sequence 8215, Ap
608	11.6	40.0	63	1	US-08-443-976-46	Sequence 46, Appl	c 681	11.4	39.3	38	4	US-09-371-772B-11756	Sequence 11756, A
609	11.6	40.0	65	1	US-08-084-718-47	Sequence 47, Appl	c 682	11.4	39.3	38	4	US-09-371-772B-12340	Sequence 12340, A
610	11.6	40.0	65	1	US-08-443-976-47	Sequence 47, Appl	c 683	11.4	39.3	38	4	US-09-371-772B-12499	Sequence 12499, A
611	11.6	40.0	65	1	US-08-443-977-47	Sequence 47, Appl	c 684	11.4	39.3	38	4	US-09-371-772B-12520	Sequence 12520, A

C 685	11.4	39.3	38	4	US-09-371-772B-12645	Sequence 12645, A	C 758	11.2	38.6	20	4	US-09-980-052-85	Sequence 85, Appl
C 686	11.4	39.3	40	4	US-09-731-466-1	Sequence 1, Appl	759	11.2	38.6	21	2	US-08-253-877C-65	Sequence 65, Appl
C 687	11.4	39.3	40	4	US-09-548-797B-170	Sequence 170, App	760	11.2	38.6	21	2	US-08-452-164A-65	Sequence 65, Appl
C 688	11.4	39.3	41	1	US-08-306-255-3	Sequence 4, Appl	761	11.2	38.6	22	4	US-09-159-871-10	Sequence 10, Appl
C 689	11.4	39.3	41	5	PCT-US93-09070-4	Sequence 4, Appl	762	11.2	38.6	22	4	US-09-375-673B-56	Sequence 56, Appl
C 690	11.4	39.3	44	1	US-10-139-842B-69	Sequence 69, Appl	C 763	11.2	38.6	24	2	US-08-747-536-28	Sequence 28, Appl
C 691	11.4	39.3	44	1	US-08-448-744-9	Sequence 9, Appl	764	11.2	38.6	24	2	US-08-332-766A-99	Sequence 99, Appl
C 692	11.4	39.3	45	1	US-08-641-638-833	Sequence 833, App	765	11.2	38.6	24	3	US-08-933-983-33	Sequence 33, Appl
C 693	11.4	39.3	46	4	US-09-338-907-231	Sequence 231, App	766	11.2	38.6	25	2	US-07-771-022P-7	Sequence 7, Appl
C 694	11.4	39.3	47	3	US-09-218-207-231	Sequence 231, App	767	11.2	38.6	25	2	US-08-257-781-5	Sequence 5, Appl
C 695	11.4	39.3	47	4	US-09-641-638-705	Sequence 705, App	C 768	11.2	38.6	25	2	US-08-827-998-1095	Sequence 1095, Ap
C 696	11.4	39.3	47	4	US-09-641-638-1034	Sequence 1034, Ap	769	11.2	38.6	25	4	US-09-866-108A-3196	Sequence 3196, Ap
C 697	11.4	39.3	47	4	US-09-641-638-1090	Sequence 1090, Ap	770	11.2	38.6	25	4	US-09-866-108A-3197	Sequence 3197, Ap
C 698	11.4	39.3	47	4	US-09-671-317-514	Sequence 514, App	771	11.2	38.6	25	5	PCT-US95-06857-5	Sequence 5, Appl
C 699	11.4	39.3	47	4	US-09-671-317-935	Sequence 935, App	C 772	11.2	38.6	25	5	PCT-US95-06857-5	Sequence 5, Appl
C 700	11.4	39.3	47	4	US-09-422-978-75	Sequence 75, Appl	773	11.2	38.6	26	1	US-08-160-861-5	Sequence 5, Appl
C 701	11.4	39.3	47	4	US-09-422-978-355	Sequence 355, App	C 774	11.2	38.6	26	1	US-08-542-363-5	Sequence 5, Appl
C 702	11.4	39.3	47	4	US-09-422-978-386	Sequence 386, App	775	11.2	38.6	26	3	US-09-100-089-5	Sequence 5, Appl
C 703	11.4	39.3	47	4	US-09-422-978-1028	Sequence 1028, Ap	C 776	11.2	38.6	26	3	US-09-100-089-5	Sequence 5, Appl
C 704	11.4	39.3	47	4	US-09-422-978-1135	Sequence 1135, Ap	C 777	11.2	38.6	26	3	US-09-311-260-136	Sequence 136, App
C 705	11.4	39.3	47	4	US-09-422-978-2273	Sequence 2273, Ap	C 778	11.2	38.6	26	4	US-09-670-827-5	Sequence 5, Appl
C 706	11.4	39.3	47	4	US-09-422-978-2469	Sequence 2469, Ap	C 779	11.2	38.6	27	4	US-08-584-040-3514	Sequence 3514, Ap
C 707	11.4	39.3	47	4	US-09-422-978-2567	Sequence 2567, Ap	C 780	11.2	38.6	28	3	US-08-867-902P-8	Sequence 8, Appl
C 708	11.4	39.3	47	4	US-09-422-978-3197	Sequence 3197, Ap	C 781	11.2	38.6	30	1	US-08-182-530-4	Sequence 4, Appl
C 709	11.4	39.3	47	4	US-09-422-978-3582	Sequence 3582, Ap	C 782	11.2	38.6	30	1	US-08-527-097-3	Sequence 3, Appl
C 710	11.4	39.3	47	4	US-09-422-978-3715	Sequence 3715, Ap	C 783	11.2	38.6	30	1	US-08-050-058B-4	Sequence 4, Appl
C 711	11.4	39.3	48	1	US-08-119-773-13	Sequence 13, Appl	C 784	11.2	38.6	30	2	US-08-463-587A-4	Sequence 4, Appl
C 712	11.4	39.3	48	1	US-08-897-956A-31	Sequence 31, Appl	C 785	11.2	38.6	30	2	US-08-463-587A-4	Sequence 4, Appl
C 713	11.4	39.3	49	4	US-09-554-929-68	Sequence 68, Appl	C 786	11.2	38.6	30	2	US-08-441-871-8	Sequence 8, Appl
C 714	11.4	39.3	50	4	US-09-554-929-127	Sequence 127, App	C 787	11.2	38.6	30	2	US-08-629-001A-110	Sequence 110, App
C 715	11.4	39.3	50	4	US-09-554-929-127	Sequence 127, App	C 788	11.2	38.6	30	3	US-08-923-854-4	Sequence 4, Appl
C 716	11.4	39.3	51	4	US-08-083-304-13	Sequence 13, Appl	C 789	11.2	38.6	30	3	US-08-642-274D-189	Sequence 189, App
C 717	11.4	39.3	51	3	US-08-911-894-63	Sequence 63, Appl	C 790	11.2	38.6	30	5	PCT-US91-03133-4	Sequence 4, Appl
C 718	11.4	39.3	56	4	US-09-724-916A-75	Sequence 75, Appl	C 791	11.2	38.6	31	1	US-08-390-850-236	Sequence 236, App
C 719	11.4	39.3	56	4	US-09-724-916A-76	Sequence 76, Appl	C 792	11.2	38.6	31	1	US-08-390-850-237	Sequence 237, App
C 720	11.4	39.3	60	1	US-08-256-964A-7	Sequence 7, Appl	C 793	11.2	38.6	31	1	US-08-323-531-71	Sequence 71, Appl
C 721	11.4	39.3	60	3	US-08-911-894-64	Sequence 64, Appl	C 794	11.2	38.6	31	1	US-08-435-634-236	Sequence 236, App
C 722	11.4	39.3	63	4	US-09-402-532-41	Sequence 41, Appl	C 795	11.2	38.6	31	1	US-08-435-634-237	Sequence 237, App
C 723	11.4	39.3	63	4	US-09-680-420A-23	Sequence 23, Appl	C 796	11.2	38.6	31	1	US-08-198-094-71	Sequence 71, Appl
C 724	11.4	39.3	63	4	US-09-621-976-18733	Sequence 18733, A	C 797	11.2	38.6	31	3	US-08-480-640A-119	Sequence 119, App
C 725	11.4	39.3	64	1	US-08-144-212-7	Sequence 7, Appl	C 798	11.2	38.6	31	3	US-08-295-802-119	Sequence 119, App
C 726	11.4	39.3	64	1	US-08-306-285-2	Sequence 14, Appl	C 799	11.2	38.6	31	3	US-08-107-794A-71	Sequence 71, Appl
C 727	11.4	39.3	67	1	US-08-306-285-2	Sequence 2, Appl	C 800	11.2	38.6	31	3	US-08-488-237A-119	Sequence 119, App
C 728	11.4	39.3	69	3	US-07-927-391-10	Sequence 10, Appl	C 801	11.2	38.6	31	4	US-08-375-992A-119	Sequence 119, App
C 729	11.4	39.3	70	1	US-08-217-210B-8	Sequence 8, Appl	C 802	11.2	38.6	31	4	US-09-206-898-22	Sequence 22, Appl
C 730	11.4	39.3	70	3	US-09-364-380-29	Sequence 29, Appl	C 803	11.2	38.6	31	4	US-09-495-052-47	Sequence 47, Appl
C 731	11.4	39.3	70	4	US-09-621-976-13621	Sequence 12621, A	C 804	11.2	38.6	31	4	US-08-472-678H-119	Sequence 119, App
C 732	11.4	39.3	71	4	US-08-956-171E-2239	Sequence 2239, Ap	C 805	11.2	38.6	31	4	US-09-247-890-4	Sequence 4, Appl
C 733	11.4	39.3	71	4	US-08-956-171E-1716	Sequence 1716, Ap	C 806	11.2	38.6	31	4	US-09-724-969-4	Sequence 4, Appl
C 734	11.4	39.3	79	3	US-08-932-082-12	Sequence 12, Appl	C 807	11.2	38.6	31	4	US-09-724-852-4	Sequence 12, Appl
C 735	11.4	39.3	79	4	US-09-861-687-12	Sequence 12, Appl	C 808	11.2	38.6	31	4	US-10-112-802-10	Sequence 10, Appl
C 736	11.4	39.3	80	1	US-08-472-255A-133	Sequence 133, App	C 809	11.2	38.6	31	4	PCT-US93-07424-71	Sequence 71, Appl
C 737	11.4	39.3	80	1	US-08-479-724A-133	Sequence 133, App	C 810	11.2	38.6	31	5	PCT-US95-02087-71	Sequence 71, Appl
C 738	11.4	39.3	80	3	US-08-479-724A-133	Sequence 133, App	C 811	11.2	38.6	31	5	PCT-US95-02087-71	Sequence 71, Appl
C 739	11.4	39.3	80	3	US-08-479-724A-133	Sequence 133, App	C 812	11.2	38.6	33	1	US-08-201-118-25	Sequence 21, Appl
C 740	11.4	39.3	80	4	US-09-849-928-133	Sequence 133, App	C 813	11.2	38.6	33	1	US-08-201-118-25	Sequence 21, Appl
C 741	11.4	39.3	80	5	PCT-US96-09455A-133	Sequence 133, App	C 814	11.2	38.6	33	2	US-08-238-821B-15	Sequence 15, Appl
C 742	11.2	38.6	17	1	US-08-373-124A-1793	Sequence 1793, Ap	C 815	11.2	38.6	33	2	US-08-238-821B-21	Sequence 21, Appl
C 743	11.2	38.6	17	1	US-08-373-124A-1797	Sequence 1797, Ap	C 816	11.2	38.6	33	3	US-09-121-425-10	Sequence 10, Appl
C 744	11.2	38.6	17	1	US-08-435-628-1793	Sequence 1793, Ap	C 817	11.2	38.6	33	3	US-09-344-700-28	Sequence 28, Appl
C 745	11.2	38.6	17	1	US-08-435-628-1797	Sequence 1797, Ap	C 818	11.2	38.6	33	4	US-09-265-653-7	Sequence 7, Appl
C 746	11.2	38.6	17	4	US-09-371-772B-5131	Sequence 5131, Ap	C 819	11.2	38.6	33	4	US-09-634-493A-10	Sequence 10, Appl
C 747	11.2	38.6	17	4	US-09-371-772B-5132	Sequence 5132, Ap	C 820	11.2	38.6	33	4	US-09-684-855-99	Sequence 99, Appl
C 748	11.2	38.6	17	4	US-09-827-998-280	Sequence 280, App	C 821	11.2	38.6	33	4	US-09-563-997A-28	Sequence 28, Appl
C 749	11.2	38.6	20	2	US-08-258-1730-18	Sequence 18, Appl	C 822	11.2	38.6	33	5	PCT-US95-05744-15	Sequence 15, Appl
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C 752	11.2	38.6	20	3	US-09-428-584-85	Sequence 86, Appl	C 825	11.2	38.6	34	3	US-08-793-666-5	Sequence 81, Appl
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C 754	11.2	38.6	20	3	US-09-499-080-18	Sequence 18, Appl	C 827	11.2	38.6	34	4	US-09-693-542-81	Sequence 2, Appl
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831	11.2	38.6	35	4	US-09-342-299-8	Sequence 8, Appli	c 904	11.2	38.6	38	4	US-09-371-772B-8225	Sequence 8225, Ap
832	11.2	38.6	35	5	PCT-US92-06821A-51	Sequence 51, Appl	c 905	11.2	38.6	38	4	US-09-371-772B-8448	Sequence 8448, Ap
833	11.2	38.6	36	1	US-08-291-932A-488	Sequence 488, App	c 906	11.2	38.6	38	4	US-09-371-772B-9921	Sequence 9921, Ap
834	11.2	38.6	36	1	US-08-334-847-163	Sequence 163, App	c 907	11.2	38.6	38	4	US-09-371-772B-10078	Sequence 10078, A
835	11.2	38.6	36	1	US-08-334-847-228	Sequence 228, App	c 908	11.2	38.6	38	4	US-09-371-772B-10731	Sequence 10731, A
836	11.2	38.6	36	1	US-08-334-847-375	Sequence 375, App	c 909	11.2	38.6	38	4	US-09-371-772B-10736	Sequence 10736, A
837	11.2	38.6	36	1	US-08-334-847-391	Sequence 391, App	c 910	11.2	38.6	38	4	US-09-371-772B-10907	Sequence 10907, A
838	11.2	38.6	36	1	US-08-334-847-745	Sequence 745, App	c 911	11.2	38.6	39	3	US-08-968-563-47	Sequence 47, Appl
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843	11.2	38.6	36	1	US-08-363-240A-286	Sequence 286, App	c 916	11.2	38.6	39	4	US-09-548-797B-138	Sequence 138, App
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846	11.2	38.6	36	1	US-08-311-486C-502	Sequence 502, App	c 919	11.2	38.6	41	4	US-08-402-923A-168	Sequence 168, App
847	11.2	38.6	36	1	US-08-311-486C-979	Sequence 979, App	c 920	11.2	38.6	42	3	US-08-491-954-34	Sequence 34, Appl
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850	11.2	38.6	36	2	US-08-585-684B-486	Sequence 486, App	c 923	11.2	38.6	43	4	US-08-758-417A-248	Sequence 248, App
851	11.2	38.6	36	2	US-08-585-684B-489	Sequence 489, App	c 924	11.2	38.6	45	1	US-08-171-389-29	Sequence 29, Appl
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860	11.2	38.6	36	3	US-09-038-073-1620	Sequence 1620, Ap	c 933	11.2	38.6	47	4	US-08-641-638-748	Sequence 748, App
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862	11.2	38.6	36	3	US-09-038-073-2028	Sequence 2028, Ap	c 935	11.2	38.6	47	4	US-09-422-978-702	Sequence 702, App
863	11.2	38.6	36	4	US-09-633-043-17	Sequence 17, Appl	c 936	11.2	38.6	47	4	US-09-422-978-844	Sequence 844, App
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874	11.2	38.6	38	1	US-08-435-628-707	Sequence 707, App	c 947	11.2	38.6	47	4	US-09-422-978-3604	Sequence 3604, Ap
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879	11.2	38.6	38	1	US-08-435-628-1806	Sequence 1806, Ap	c 952	11.2	38.6	48	4	US-09-065-914B-2	Sequence 2, Appli
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Sequence 9, Appli
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60 3 US-09-046-247-47
60 4 US-09-626-929-22
60 4 US-09-484-850-22
60 4 US-09-408-392-22

ALIGNMENTS

RESULT 1
US-08-667-079B-5/C
; Sequence 5, Application US/08667079B
; Patent No. 5789171
; GENERAL INFORMATION:
; APPLICANT: Mark S. Smeltzer
; TITLE OF INVENTION: Use of cna, fnbA, fnbB, and hlb Gene Probes for the Strain-Sp
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Benjamin Aaron Adler, MCGREGOR & ADLER, P.C.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,079B
; FILING DATE: June 20, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Benjamin Aaron
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
US-08-667-079B-5
Query Match 52.4%; Score 15.2; DB 1; Length 33;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 12; Conservative 8; Indels 0; Gaps 0;
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Db 32 ATGATGTTTATTAGTTCCTCCCGGCT 5
RESULT 2
US-09-422-978-1097
; Sequence 1097, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET-020CE1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1097
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2043-220 : polymorphic base A or T
US-09-422-978-1097
Query Match 52.4%; Score 15.2; DB 4; Length 47;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
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Db 15 AGACTCTTTWTGTACCTCCCA 36
RESULT 3
US-07-971-101-6/c
; Sequence 6, Application US/07971101
; Patent No. 5443969
; GENERAL INFORMATION:
; APPLICANT: Wilson, Thomas M.A. et al.
; TITLE OF INVENTION: RNA Packaging System
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,101
; FILING DATE: 19921029
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7108-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: RNA
; US-07-971-101-6

Query Match 52.4%; Score 15.2; DB 1; Length 75;
Best Local Similarity 53.6%; Pred. No. 4.7e+02;
Matches 15; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAGAUCUUUUGUAGCCCAAGGCG 28
Db 41 AACGACTTCTCTGTAAGTCCATGGCG 14

RESULT 4
US-08-219-633-25/c
; Sequence 25, Application US/08219633
; Patent No. 5599666
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Pueris, Christoph
; TITLE OF INVENTION: ALLELIC LADDERS FOR SHORT TANDEM REPEAT
; TITLE OF INVENTION: LOCI
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 15-AUG-1995
; APPLICATION NUMBER: US/08/515,236
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,633
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-219-633-25

Query Match 51.0%; Score 14.8; DB 1; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUCUUUUUGUAGCCCAAGGCGU 29
Db 29 GATTATTCTTATCATCCACTAGGCT 4

RESULT 6
US-08-761-950-25/c
; Sequence 25, Application US/08761950
; Patent No. 5783406
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Pueris, Christoph
; TITLE OF INVENTION: ALLELIC LADDERS FOR SHORT TANDEM REPEAT
; TITLE OF INVENTION: LOCI
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: One South Pinckney Street, P.O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/219,633
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-219-633-25

Query Match 51.0%; Score 14.8; DB 1; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUCUUUUUGUAGCCCAAGGCGU 29
Db 29 GATTATTCTTATCATCCACTAGGCT 4

RESULT 6
US-08-761-950-25/c
; Sequence 25, Application US/08761950
; Patent No. 5783406
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Pueris, Christoph
; TITLE OF INVENTION: ALLELIC LADDERS FOR SHORT TANDEM REPEAT
; TITLE OF INVENTION: LOCI
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: One South Pinckney Street, P.O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 15-AUG-1995
; APPLICATION NUMBER: US/08/515,236
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,633
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-515-236-25

Query Match 51.0%; Score 14.8; DB 1; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUCUUUUUGUAGCCCAAGGCGU 29
Db 29 GATTATTCTTATCATCCACTAGGCT 4
```

```

; Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUCUUUUUGUAGCCCAAGGCGU 29
Db 29 GATTATTCTTATCATCCACTAGGCT 4

RESULT 5
US-08-515-236-25/c
; Sequence 25, Application US/08515236
; Patent No. 5674686
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Pueris, Christoph
; TITLE OF INVENTION: ALLELIC LADDERS FOR SHORT TANDEM REPEAT
; TITLE OF INVENTION: LOCI
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: One South Pinckney Street, P.O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/515,236
; FILING DATE: 15-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,633
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-515-236-25

Query Match 51.0%; Score 14.8; DB 1; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUCUUUUUGUAGCCCAAGGCGU 29
Db 29 GATTATTCTTATCATCCACTAGGCT 4

RESULT 6
US-08-761-950-25/c
; Sequence 25, Application US/08761950
; Patent No. 5783406
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Pueris, Christoph
; TITLE OF INVENTION: ALLELIC LADDERS FOR SHORT TANDEM REPEAT
; TITLE OF INVENTION: LOCI
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: One South Pinckney Street, P.O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 15-AUG-1995
; APPLICATION NUMBER: US/08/515,236
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,633
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-515-236-25

Query Match 51.0%; Score 14.8; DB 1; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUCUUUUUGUAGCCCAAGGCGU 29
Db 29 GATTATTCTTATCATCCACTAGGCT 4
```

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; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,950
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/515,236
; FILING DATE: 15-AUG-1995
; APPLICATION NUMBER: US 08/219,633
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-761-950-25

Query Match 51.0%; Score 14.8; DB 1; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGGCU 29
Db 29 GATTATCTTATCATCCACTAGGCT 4

RESULT 7
US-08-632-575B-39/c
; Sequence 39, Application US/08632575B
; Patent No. 5843660
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; TITLE OF INVENTION: Multiplex Amplification of
; TITLE OF INVENTION: Short Tandem Repeat Loci
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: DOS, version 6.0
; SOFTWARE: WordPerfect 5.1 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,575B
; FILING DATE: 04/15/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,544
; FILING DATE: 09/30/94
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29

; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/327,229
; FILING DATE: 07-Jun-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,544
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-327-229-31

Query Match 51.0%; Score 14.8; DB 3; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGGCU 29
Db 29 GATTATCTTATCATCCACTAGGCT 4

RESULT 9
US-09-199-542B-39/c
```

```
; Sequence 39, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)
; SEQ ID NO 39
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: HUMWPA31
US-09-199-542B-39

Query Match 51.0%; Score 14.8; DB 4; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGAAGCCCAAGGCGCU 29
DB 29 GATTATTCCTTATCATCCACTAGGGCT 4

RESULT 10
PCT-US95-12608-31/c
; Sequence 31, Application PC/TUS9512608
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; APPLICANT: Lins, Ann M.
; TITLE OF INVENTION: MULTIPLEX AMPLIFICATION OF SHORT TANDEM
; TITLE OF INVENTION: REPEAT LOCI
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: P. O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12608
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-12608-31

; Sequence 39, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)
; SEQ ID NO 39
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: HUMWPA31
US-09-199-542B-39

Query Match 51.0%; Score 14.8; DB 4; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGAAGCCCAAGGCGCU 29
DB 29 GATTATTCCTTATCATCCACTAGGGCT 4

RESULT 11
US-08-632-575B-59/c
; Sequence 59, Application US/08632575B
; Patent No. 5843660
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; TITLE OF INVENTION: Multiplex Amplification of
; TITLE OF INVENTION: Short Tandem Repeat Loci
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: DOS, version 6.0
; SOFTWARE: WordPerfect 5.1 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,575B
; FILING DATE: 04/15/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,544
; FILING DATE: 09/30/94
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; POSITION IN GENOME:
; MAP POSITION: HUMWPA31
US-08-632-575B-59

Query Match 51.0%; Score 14.8; DB 2; Length 32;
Best Local Similarity 42.3%; Pred. No. 6.1e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGAAGCCCAAGGCGCU 29
DB 29 GATTATTCCTTATCATCCACTAGGGCT 4

RESULT 12
US-09-199-542B-59/c
; Sequence 59, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)
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; SEQ ID NO 59
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: HUMVFA31
US-09-199-542B-59

Query Match
Best Local Similarity 51.0%; Score 14.8; DB 4; Length 32;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGGCT 29
||: : : : |||
29 GATTATCTTATCATCCACTAGGCT 4

RESULT 13
US-09-063-733A-18
; Sequence 18, Application US/09063733A
; Patent No. 6372211
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,733A
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOST:022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-787-1440
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-063-733A-18

Query Match
Best Local Similarity 50.3%; Score 14.6; DB 4; Length 25;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUGUAGCCCC 22
||| : : : |||
5 AAGCTTCTCTTGTATATACC 25

Db

RESULT 14
US-08-486-969-46/c
; Sequence 46, Application US/08486969
; Patent No. 5843456
; GENERAL INFORMATION:
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; APPLICANT: Paoletti, Enzo
; APPLICANT: Maki, Joanne
; TITLE OF INVENTION: RECOMBINANT POXVIRUS - RABIES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,969
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-486-969-46

Query Match
Best Local Similarity 50.3%; Score 14.6; DB 2; Length 53;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 9 UUUUUGUAGCCCAAGGCT 29
||||: |||
Db 29 TTTTGTAGCTTCCCGGCT 9

RESULT 15
US-09-827-998-1098/c
; Sequence 1098, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 1098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1098

Query Match
Best Local Similarity 49.0%; Score 14.2; DB 4; Length 25;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
```


Qy 7 UCUUUUGUAGCCCAAG 25
:|||||:
Db 25 TCTTTTGTAGTCCCAAG 7

RESULT 16

US-09-827-998-1099/c
; Sequence 1099, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 1099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1099

Query Match 49.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 7 UCUUUUGUAGCCCAAG 25
:|||||:
Db 24 TCTTTTGTAGTCCCAAG 6

RESULT 17

US-09-827-998-1100/c
; Sequence 1100, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 1100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1100

Query Match 49.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 7 UCUUUUGUAGCCCAAG 25
:|||||:
Db 23 TCTTTTGTAGTCCCAAG 5

RESULT 18

US-09-827-998-1103/c
; Sequence 1103, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

US-09-827-998-1101/c
; Sequence 1101, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 1101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1101

Query Match 49.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 7 UCUUUUGUAGCCCAAG 25
:|||||:
Db 22 TCTTTTGTAGTCCCAAG 4

RESULT 19

US-09-827-998-1102/c
; Sequence 1102, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 1102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1102

Query Match 49.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 7 UCUUUUGUAGCCCAAG 25
:|||||:
Db 21 TCTTTTGTAGTCCCAAG 3

RESULT 20

US-09-827-998-1103/c
; Sequence 1103, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

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; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 96
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12847-37 : polymorphic base A or G
US-09-422-978-96

Query Match          49.0%; Score 14.2; DB 4; Length 47;
Best Local Similarity 42.9%; Pred.No. 1.2e+03;
Matches 9; Conservative 8; Mismatches 4; Indels

Qy 9 UUUUUGAAGCCCAAGGCU 29
      :::::|||||:::::
Db 8 TTTTCTAAGGTCCACRGCT 28

RESULT 23
US-08-410-654B-30
; Sequence 30, Application US/08410654B
; Patent No. 5833976
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Anne O'Garra
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of Interleukin-10 to Treat
; TITLE OF INVENTION: Septic Shock
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,654B
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,854
; FILING DATE: 19-APR-1994
; APPLICATION NUMBER: US 07/926,853
; FILING DATE: 06-AUG-1992
; APPLICATION NUMBER: US 07/742,129
; FILING DATE: 06-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: DX0221KQ1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-410-654B-30

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Query Match 49.0%; Score 14.2; DB 2; Length 69;
Best Local Similarity 51.9%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAGAUAUUUUUUAAGCCCAAGG 27
Db 7 AAGAATGCCTTTAATAAGCTCCAAG 33

RESULT 24

US-08-474-851-30
; Sequence 30, Application US/08474851
; Patent No. 5837232
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Anne O'Garra
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat
; TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,851
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1GD
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)

US-08-474-851-30

Query Match 49.0%; Score 14.2; DB 2; Length 69;
Best Local Similarity 51.9%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAGAUAUUUUUUAAGCCCAAGG 27
Db 7 AAGAATGCCTTTAATAAGCTCCAAG 33

RESULT 25

US-08-481-560-30
; Sequence 30, Application US/08481560
; Patent No. 5837293
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Anne O'Garra
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of Interleukin-10 to Modulate
; TITLE OF INVENTION: Inflammation or T-Cell Mediated
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,560
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1GC
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)

US-08-481-560-30

Query Match 49.0%; Score 14.2; DB 2; Length 69;
Best Local Similarity 51.9%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAGAUAUUUUUUAAGCCCAAGG 27
Db 7 AAGAATGCCTTTAATAAGCTCCAAG 33

RESULT 26

US-09-571-774-2
; Sequence 2, Application US/09571774
; Patent No. 6479262
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; TITLE OF INVENTION: Solid Phase Enzymatic Assembly of Polynucleotides
; FILE REFERENCE: HER-0005
; CURRENT APPLICATION NUMBER: US/09/571,774
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 4

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Oligonucleotide
US-09-571-774-2

Query Match          49.3%; Score 14; DB 4; Length 41;
Best Local Similarity 54.5%; Pred. No. 1.5e+03;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAUCUUUUUUUAAGCCCAAA 24
      |||||:|:|:|:|:|:|:|:|:|
Db      15 AGATTCCTCGTTAGCCCAAA 36

RESULT 27
US-09-852-385-2
; Sequence 2, Application US/09852385
; Patent No. 6635453
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; TITLE OF INVENTION: Methods For The Enzymatic Assembly Of Polynucleotides And Identification Of Polynucleotides Having Desired Characteristics
; FILE REFERENCE: HER-0042
; CURRENT APPLICATION NUMBER: US/09/852,385
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/571,774
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6635453el Sequence
US-09-852-385-2

Query Match          48.3%; Score 14; DB 4; Length 41;
Best Local Similarity 54.5%; Pred. No. 1.5e+03;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAUCUUUUUUUAAGCCCAAA 24
      |||||:|:|:|:|:|:|:|:|:|
Db      15 AGATTCCTCGTTAGCCCAAA 36

RESULT 28
US-08-943-731-336/c
; Sequence 336, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISSA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
```

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; STREET: ELR.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-336

Query Match          47.6%; Score 13.8; DB 3; Length 25;
Best Local Similarity 47.1%; Pred. No. 1.7e+03;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      5 AUUCUUUUUUUAAGCCC 21
      |||||:|:|:|:|:|:|
Db      22 ATTCTCTTGTGAGCCC 6

RESULT 29
US-09-199-542B-76/c
; Sequence 76, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)
; SEQ ID NO 76
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: HUMWFA31
US-09-199-542B-76

Query Match          47.6%; Score 13.8; DB 4; Length 33;
Best Local Similarity 44.0%; Pred. No. 1.8e+03;
Matches 11; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
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RESULT 36
US-09-422-978-1843/c
; Sequence 1843, Application US/09422978
; Patent No. 6537751

us-09-310-844c-25.max.rni

Tue Apr 20 10:03:05 2004

Search completed: April 18, 2004, 10:00:00
Job time : 42.6667 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:30:54 ; Search time 1527.67 Seconds

(without alignments)
566.880 Million cell updates/sec

Title: US-09-310-844C-25

Perfect score: 29

Sequence: 1 aaagaucuuuuuuuaagcccaaggcu 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 375216

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estm.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hcc.*

9: gb_est1.*

10: gb_est2.*

11: gb_hcc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	17.4	60.0	67	9	AA708911 z164a10.s
C 3	16.6	57.2	70	9	AI609394 tw93b03.x
C 4	16.6	57.2	75	14	H07686 khg012 BNL

C 5	16	55.2	51	12	BG361927
C 6	16	55.2	73	12	BG361878
C 7	15.8	54.5	58	9	AI824019 wj29f03.x
C 8	15.8	54.5	72	13	BG613481 id07h06.y
C 9	15.8	54.5	76	28	AQ657549 IM0533u18
C 10	15.6	53.8	37	9	AI802260 tj36g07.x
C 11	15.6	53.8	58	28	AZ834846 2M0117F18
C 12	15.4	53.1	47	14	U44334
C 13	15.4	53.1	79	28	BH252676
C 14	15.4	53.1	78	29	AG260396
C 15	15.2	52.4	61	9	AI318033
C 16	15.2	52.4	65	12	BM517546
C 17	15.2	52.4	78	9	AA936218
C 18	15.1	51.7	58	28	B02943
C 19	15.1	51.7	68	14	CD682098
C 20	14.8	51.0	34	28	AZ840876
C 21	14.8	51.0	49	28	AZ576537
C 22	14.8	51.0	55	9	AI224478
C 23	14.8	51.0	64	10	BE636255
C 24	14.8	51.0	67	29	CG588850
C 25	14.8	51.0	70	9	AL780467
C 26	14.8	51.0	76	28	B289798
C 27	14.8	51.0	77	29	CG549254
C 28	14.6	50.3	52	29	BX650715
C 29	14.6	50.3	53	29	AL940874
C 30	14.6	50.3	59	10	BE970792
C 31	14.6	50.3	61	13	BQ479345
C 32	14.6	50.3	65	29	AL763793
C 33	14.6	50.3	69	28	BZ768797
C 34	14.6	50.3	70	28	BZ768791
C 35	14.6	50.3	70	28	BZ768795
C 36	14.6	50.3	71	14	CE227161
C 37	14.6	50.3	71	28	AZ833202
C 38	14.6	50.3	75	9	AI696772
C 39	14.6	50.3	80	29	AL770832
C 40	14.6	50.3	80	29	BX662819
C 41	14.4	49.7	35	28	BH856246
C 42	14.4	49.7	35	28	BH856247
C 43	14.4	49.7	37	28	BH856247
C 44	14.4	49.7	41	28	AZ598587
C 45	14.4	49.7	51	14	CF425249
C 46	14.4	49.7	51	29	DMES45740
C 47	14.4	49.7	56	28	BZ665747
C 48	14.4	49.7	57	12	BG362067
C 49	14.4	49.7	58	9	AV953887
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C 51	14.4	49.7	65	28	BH908271
C 52	14.4	49.7	66	12	BG361679
C 53	14.4	49.7	66	29	CG485985
C 54	14.4	49.7	67	28	BH848343
C 55	14.4	49.7	67	29	CC517699
C 56	14.4	49.7	67	29	CG474006
C 57	14.4	49.7	67	29	CG474744
C 58	14.4	49.7	67	29	CG475921
C 59	14.4	49.7	67	29	CG476132
C 60	14.4	49.7	67	29	CG476312
C 61	14.4	49.7	67	29	CG476342
C 62	14.4	49.7	67	29	CG476917
C 63	14.4	49.7	67	29	CG477123
C 64	14.4	49.7	67	29	CG477690
C 65	14.4	49.7	67	29	CG477783
C 66	14.4	49.7	67	29	CG479801
C 67	14.4	49.7	67	29	CG480240
C 68	14.4	49.7	67	29	CG480439
C 69	14.4	49.7	67	29	CG480503
C 70	14.4	49.7	67	29	CG480672
C 71	14.4	49.7	67	29	CG480879
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C 73	14.4	49.7	67	29	CG480982
C 74	14.4	49.7	67	29	CG481136
C 75	14.4	49.7	67	29	CG481158
C 76	14.4	49.7	67	29	CG481469
C 77	14.4	49.7	67	29	CG482313

C 78	14.4	49.7	67	29	CG482838	OST16124	CG482838	OST16124	151	14.4	49.7	72	29	EX224205	Danio rer
C 79	14.4	49.7	67	29	CG482887	OST16195	CG482887	OST16195	152	14.4	49.7	73	12	BM568281	sal102402.
C 80	14.4	49.7	67	29	CG482965	OST16319	CG482965	OST16319	153	14.4	49.7	74	29	CG574740	OST207881
C 81	14.4	49.7	67	29	CG483071	OST18504	CG483071	OST18504	C 154	14.4	49.7	76	12	BG361288	gb56a08.Y
C 82	14.4	49.7	67	29	CG484155	OST18008	CG484155	OST18008	C 155	14.4	49.7	76	13	BQ393681	BQ393681
C 83	14.4	49.7	67	29	CG484480	OST18444	CG484480	OST18444	C 156	14.4	49.7	76	28	AQ025263	AQ025263
C 84	14.4	49.7	67	29	CG484698	OST18749	CG484698	OST18749	C 157	14.4	49.7	77	14	CS262321	CS262321
C 85	14.4	49.7	67	29	CG484811	OST18895	CG484811	OST18895	C 158	14.4	49.7	78	13	BQ244462	BQ244462
C 86	14.4	49.7	67	29	CG484964	OST19117	CG484964	OST19117	C 159	14.4	49.7	78	28	BH044967	BH044967
C 87	14.4	49.7	67	29	CG485056	OST19253	CG485056	OST19253	C 160	14.4	49.7	80	29	CG570907	CG570907
C 88	14.4	49.7	67	29	CG485118	OST19344	CG485118	OST19344	C 161	14.2	49.0	38	29	BZ355014	BZ355014
C 89	14.4	49.7	67	29	CG485130	OST19361	CG485130	OST19361	C 162	14.2	49.0	40	29	CG779591	CG779591
C 90	14.4	49.7	67	29	CG485219	OST19496	CG485219	OST19496	C 163	14.2	49.0	40	29	BQ5408	BQ5408
C 91	14.4	49.7	67	29	CG485496	OST19923	CG485496	OST19923	C 164	14.2	49.0	54	28	AZ38752	AZ38752
C 92	14.4	49.7	67	29	CG486069	OST20815	CG486069	OST20815	C 165	14.2	49.0	59	14	CH258816	CH258816
C 93	14.4	49.7	67	29	CG486451	OST21486	CG486451	OST21486	C 166	14.2	49.0	62	29	CG559308	CG559308
C 94	14.4	49.7	67	29	CG486698	OST21859	CG486698	OST21859	C 167	14.2	49.0	64	29	EX161966	EX161966
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C 112	14.4	49.7	67	29	CG489219	OST25655	CG489219	OST25655	C 185	14.2	49.0	67	9	AU265792	AU265792
C 113	14.4	49.7	67	29	CG489435	OST26024	CG489435	OST26024	C 186	14.2	49.0	67	14	CB261630	CB261630
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C 116	14.4	49.7	67	29	CG489701	OST26526	CG489701	OST26526	C 189	14.2	49.0	76	9	AI633915	AI633915
C 117	14.4	49.7	67	29	CG489883	OST26861	CG489883	OST26861	C 190	14.2	49.0	80	29	AI797155	AI797155
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C 147	14.4	49.7	67	29	CG507869	OST58051	CG507869	OST58051	C 220	13.8	47.6	64	29	CG626740	CG626740
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370	13.2	45.5	75	14	CK098783	AK011P73.5	C 443	13	44.8	78	29	CG482517	OST15648
371	13.2	45.5	75	29	CG526082	OST102290	C 444	13	44.8	78	29	CG491713	OST29242
C 372	13.2	45.5	76	9	AB691060	v57b12.s	C 445	13	44.8	79	9	AA461918	v595h10.r
C 373	13.2	45.5	76	9	AA938354	on71c08.s	C 446	13	44.8	79	12	CG314684	OP1.0.189
C 374	13.2	45.5	76	9	AA938354	on71c08.s	C 447	13	44.8	79	14	W89294	mf62h03.r1
C 375	13.2	45.5	76	10	AW194637	AW194637	C 448	13	44.8	79	29	CG477179	OST96975.M
C 376	13.2	45.5	76	28	AZ482846	IM0308E08	C 449	13	44.8	79	29	CG483993	OST17785
C 377	13.2	45.5	77	13	BU652110	1112097E1	C 450	13	44.8	79	29	CG485151	OST19390
C 378	13.2	45.5	77	14	T474577	YC57c02.s1	C 451	13	44.8	79	29	CG485511	OST19948
C 379	13.2	45.5	77	14	AF067770	AF067770	C 452	13	44.8	79	29	CG486032	OST20752
C 380	13.2	45.5	77	28	BH907776	SALK_0440	C 453	13	44.8	80	28	BH901319	SALK_0744
C 381	13.2	45.5	78	28	BH252197	SALK_0129	C 454	13	44.8	80	29	CG486056	OST20793
C 382	13.2	45.5	78	29	DR24P18T	DR24P18T	C 455	13	44.8	80	29	CG486058	ArabiDops
C 383	13.2	45.5	79	9	AA144854	AA144854	C 456	12.8	44.1	32	28	AZ760558	IM0554320
C 384	13.2	45.5	79	28	AZ828847	mr73C08.r	C 457	12.8	44.1	33	28	BH791695	SALK_0608
C 385	13.2	45.5	80	9	AJ499317	AJ499317	C 458	12.8	44.1	34	12	BJ055305	BJ055305
C 386	13.2	45.5	80	14	N36623	YX88d04.r1	C 459	12.8	44.1	36	28	AZ469569	IM0283F07
C 387	13.2	45.5	80	28	BZ357801	BZ357801	C 460	12.8	44.1	37	29	AL951243	ArabiDops
C 388	13	44.8	22	14	D18745	MUSGS01807	C 461	12.8	44.1	39	10	BF538245	602053723
C 389	13	44.8	30	28	AZ780490	2M0017G24	C 462	12.8	44.1	39	12	BJ060351	BJ060351
C 390	13	44.8	35	29	AL939013	ArabiDops	C 463	12.8	44.1	40	9	AA872575	calsh08.s
C 391	13	44.8	38	29	AG205629	Oryza sat	C 464	12.8	44.1	42	28	AZ586660	IM0392B17
C 392	13	44.8	47	10	AW333805	S26D6 AGS	C 465	12.8	44.1	42	28	BH865434	SALK_0985
C 393	13	44.8	49	28	AZ622361	1M0459B09	C 466	12.8	44.1	43	28	AZ597048	IM0410K10
C 394	13	44.8	50	9	AU105337	AU105337	C 467	12.8	44.1	43	29	EX659541	ArabiDops
C 395	13	44.8	50	9	AU105351	AU105351	C 468	12.8	44.1	43	29	EX659541	ArabiDops
C 396	13	44.8	51	13	EQ593814	EQ593814	C 469	12.8	44.1	44	28	BH789804	ArabiDops
C 397	13	44.8	51	12	BI845578	BI845578	C 470	12.8	44.1	44	28	AL771575	ArabiDops
C 398	13	44.8	54	28	BH863662	SALK_0943	C 471	12.8	44.1	47	29	EX201354	Danilo rer
C 399	13	44.8	56	9	A1656187	A1656187	C 472	12.8	44.1	48	28	BH747043	SALK_0093
C 400	13	44.8	56	28	BZ382500	SALK_1183	C 473	12.8	44.1	48	28	BZ596082	SALK_0920
C 401	13	44.8	56	28	BZ382501	SALK_1183	C 474	12.8	44.1	49	12	B1894632	gb51a06.Y
C 402	13	44.8	56	29	AL762058	ArabiDops	C 475	12.8	44.1	52	12	BG361926	gb49d09.Y
C 403	13	44.8	57	28	BH410651	BH410651	C 476	12.8	44.1	52	12	AZ833106	2M0113M20
C 404	13	44.8	58	9	AA896470	AA896470	C 477	12.8	44.1	52	28	B00432	CSRL-112C4-
C 405	13	44.8	58	9	A1528594	A1528594	C 478	12.8	44.1	52	28	AG263226	Lotus cor
C 406	13	44.8	58	28	BH902709	BH902709	C 479	12.8	44.1	53	12	BG361338	gb66n04.Y
C 407	13	44.8	59	28	AZ800849	2M0059C02	C 480	12.8	44.1	53	12	BG362155	gb52c05.Y
C 408	13	44.8	60	29	TA129G07P	TA129G07P	C 481	12.8	44.1	53	14	CB257152	44-B01113
C 409	13	44.8	61	14	CD951024	CD951024	C 482	12.8	44.1	53	14	CF872594	tr1C031xp
C 410	13	44.8	62	13	BQ265706	BQ265706	C 483	12.8	44.1	53	28	BZ378745	SALK_1118
C 411	13	44.8	62	29	CG554686	OST188558	C 484	12.8	44.1	54	9	AA826331	of11f03.s
C 412	13	44.8	62	28	BH902683	BH902683	C 485	12.8	44.1	54	10	AW245427	2822979.3
C 413	13	44.8	64	9	A1139668	A1139668	C 486	12.8	44.1	54	12	BG362022	gb50d11.Y
C 414	13	44.8	64	28	BH814721	BH814721	C 487	12.8	44.1	54	12	B1865449	ft22h02.X
C 415	13	44.8	65	28	AZ346683	1M0082G05	C 488	12.8	44.1	55	28	BZ382010	SALK_1177
C 416	13	44.8	66	13	BQ761054	BQ761054	C 489	12.8	44.1	56	12	BG361384	gb76g07.Y
C 417	13	44.8	67	10	B5017439	B5017439	C 490	12.8	44.1	56	12	BG362337	gb70e03.Y
C 418	13	44.8	67	28	B01454	B01454	C 491	12.8	44.1	56	13	BQ587876	S013302.0
C 419	13	44.8	67	29	CG624461	OST32B242	C 492	12.8	44.1	56	14	CA482274	LuP12002E
C 420	13	44.8	68	9	A1155708	A1155708	C 493	12.8	44.1	56	28	AZ318460	IM0037J01
C 421	13	44.8	68	13	CG2494	CG2494	C 494	12.8	44.1	57	12	BG360953	gb42c05.Y
C 422	13	44.8	68	29	BX662822	BX662822	C 495	12.8	44.1	59	9	AA574548	vm29f09.r
C 423	13	44.8	69	10	AW551533	AW551533	C 496	12.8	44.1	60	12	BG361965	gb46e08.Y
C 424	13	44.8	69	28	AZ662287	AZ662287	C 497	12.8	44.1	60	14	CD945997	REH_11.Ge
C 425	13	44.8	70	28	BH216023	BH216023	C 498	12.8	44.1	61	28	AD593622	AST_1HDB2
C 426	13	44.8	70	28	BZ354128	BZ354128	C 499	12.8	44.1	62	12	BG362159	gb52d04.Y
C 427	13	44.8	70	28	BZ768793	BZ768793	C 500	12.8	44.1	62	12	BG362380	gb71b12.Y
C 428	13	44.8	71	29	CG481208	CG481208	C 501	12.8	44.1	62	12	BG408734	gb80b06.Y
C 429	13	44.8	71	29	CG520678	OST86569	C 502	12.8	44.1	62	29	AX656049	ArabiDops
C 430	13	44.8	72	12	BJ082110	BJ082110	C 503	12.8	44.1	63	10	AW264395	xr02f09.X
C 431	13	44.8	73	14	CK097081	UB38BPC12	C 504	12.8	44.1	63	12	BG362361	gb70h04.Y
C 432	13	44.8	75	9	A1801746	co94n07.X	C 505	12.8	44.1	63	12	CF328358	NAC1--03-
C 433	13	44.8	75	29	CG520478	CG520478	C 506	12.8	44.1	63	14	CG328358	NAC1--03-
C 434	13	44.8	75	29	BX653572	BX653572	C 507	12.8	44.1	64	12	BG408762	gb76f08.Y
C 435	13	44.8	76	13	BQ548400	rd25h04.Y	C 508	12.8	44.1	64	12	BM025873	OST75422
C 436	13	44.8	76	29	CG480684	CG480684	C 509	12.8	44.1	64	29	CG602220	AT1744319
C 437	13	44.8	76	29	CG487317	CG487317	C 510	12.8	44.1	65	9	AI744319	tr09d04.X
C 438	13	44.8	76	29	CG487317	OST22784	C 511	12.8	44.1	65	12	BG361984	gb46g10.Y
C 439	13	44.8	77	14	CF354398	CF354398	C 512	12.8	44.1	65	12	BM282506	ki27e03.Y
C 440	13	44.8	77	29	CG486552	OST21854	C 513	12.8	44.1	65	13	BX735697	BX735697
C 441	13	44.8	77	29	CG464392	CG464392	C 514	12.8	44.1	65	29	CG664319	OST451176
C 442	13	44.8	78	9	AA415010	vc50e05.r	C 515	12.8	44.1	65	29	BX531310	ArabiDops

C 516	12.8	44.1	66	12	BG361575	BG361575	gb54h07.y	C 589	12.6	43.4	52	28	BZ662046	BZ662046	SALK_0255
C 517	12.8	44.1	66	12	BG361936	BG361936	gb49e12.y	C 590	12.6	43.4	53	12	BG315130	BG315130	POI_0.79
518	12.8	44.1	66	14	CB817611	CB817611	d3n12pz.f	591	12.6	43.4	53	28	BH852743	BH852743	SALK_0755
519	12.8	44.1	66	29	CG518752	CG518752	OST90980	592	12.6	43.4	53	29	EX660051	EX660051	Arabidops
C 520	12.8	44.1	66	29	TA123H02P	AL463084	T. brucei	593	12.6	43.4	54	9	AA506793	EST031	Hu
C 521	12.8	44.1	67	9	AA506572	AA506572	n117407.s	594	12.6	43.4	55	10	AW698793	r379	non-
C 522	12.8	44.1	67	14	CD946435	CD946435	REN_47.Gc	C 595	12.6	43.4	55	13	BUS78287	sa50h11.	
C 523	12.8	44.1	67	28	BZ896657	BZ896657	SALK_0230	C 596	12.6	43.4	56	12	BUS78287	sa50h11.	
C 524	12.8	44.1	68	12	BG409168	BG409168	gb87c02.y	C 597	12.6	43.4	56	28	AZ449951	BJ055025	
525	12.8	44.1	68	12	BI333307	BI333307	602996669	598	12.6	43.4	57	14	CB046012	IM0204K15	
C 526	12.8	44.1	69	9	AA700612	AA700612	z141d03.s	599	12.6	43.4	57	28	AZ405121	NI0173020	
527	12.8	44.1	69	10	AW698388	AW698388	G234.Glan	C 600	12.6	43.4	58	12	BM128723	if15d09.y	
C 528	12.8	44.1	69	29	CG793901	CG793901	SALK_0196	C 601	12.6	43.4	58	12	B00509	CSRL-115b2-	
C 529	12.8	44.1	69	29	CG475794	CG475794	OSTA390.M	C 602	12.6	43.4	60	9	AI1719784	as41b08.x	
C 530	12.8	44.1	70	10	BF643300	BF643300	NF005B1E	C 603	12.6	43.4	61	9	AI189672	qd3a08.x	
C 531	12.8	44.1	70	13	C21062	C21062	HUMS000256	C 604	12.6	43.4	61	9	AA595454	na3a06.s	
C 532	12.8	44.1	70	14	CF038601	CF038601	QCH25h06.	C 605	12.6	43.4	61	9	AA612304	vn97d10.r	
533	12.8	44.1	70	29	CG718270	CG718270	1119052C0	606	12.6	43.4	61	10	BE248505	NF066C12D	
C 534	12.8	44.1	71	29	CG520384	CG520384	OST95614	C 607	12.6	43.4	61	29	CG513355	OST956685	
C 535	12.8	44.1	72	9	AA570253	AA570253	nf39e03.s	C 608	12.6	43.4	61	29	CG548659	OST150666	
C 536	12.8	44.1	72	10	BF460713	BF460713	UI-M-CGDP	C 609	12.6	43.4	62	10	AW638819	bl75a04.w	
C 537	12.8	44.1	72	10	BF462233	BF462233	UI-M-CGDP	C 610	12.6	43.4	62	29	CG474556	OST2557.M	
C 538	12.8	44.1	72	10	BF462877	BF462877	UI-M-CGDP	611	12.6	43.4	62	29	EX290641	Arabidops	
C 539	12.8	44.1	73	12	BG361017	BG361017	gb44e01.y	C 612	12.6	43.4	64	9	AI584516	ny06h06.s	
C 540	12.8	44.1	73	12	BI865610	BI865610	ft22h02.y	C 613	12.6	43.4	64	9	AI584516	fb95a02.x	
541	12.8	44.1	73	13	BQ128805	BQ128805	li23c08.y	C 614	12.6	43.4	64	10	BF118530	SMOVL3CAN	
542	12.8	44.1	73	29	CG778959	CG778959	li23c031A0	C 615	12.6	43.4	64	12	BM515149	kj65a07.y	
C 543	12.8	44.1	74	9	AA574536	AA574536	vm29e03.x	C 616	12.6	43.4	64	29	AG265379	Lotus.cor	
544	12.8	44.1	74	13	BQ265575	BQ265575	NISC_ff07	C 617	12.6	43.4	65	9	AG620913	af96b03.s	
545	12.8	44.1	74	13	BQ591165	BQ591165	S013311-0	C 618	12.6	43.4	65	14	CF885082	trico077Kh	
546	12.8	44.1	74	13	BQ672599	BQ672599	hag8002x1	619	12.6	43.4	65	28	BH810688	SALK_0510	
C 547	12.8	44.1	74	28	AZ918214	AZ918214	1006003F0	620	12.6	43.4	65	29	CG708273	1119008C1	
C 548	12.8	44.1	74	28	CG202432	CG202432	3591.1.2	621	12.6	43.4	66	14	CB053335	NISC_g113	
549	12.8	44.1	74	29	CG581504	CG581504	OST221848	622	12.6	43.4	66	28	AZ500141	IM0338016	
C 550	12.8	44.1	75	12	BG361021	BG361021	gb44e08.y	623	12.6	43.4	67	14	CB165153	86.Alfalf	
C 551	12.8	44.1	76	9	AV560198	AV560198	AV560198	624	12.6	43.4	67	14	CB357125	ZF001-P00	
C 552	12.8	44.1	76	29	CG562220	CG562220	OST360383	625	12.6	43.4	67	14	CF278112	145TL-03	
553	12.8	44.1	76	29	CG565682	CG565682	OST429400	C 626	12.6	43.4	67	29	CG543322	OST139031	
554	12.8	44.1	77	9	AA037767	AA037767	mc10h01.r	C 627	12.6	43.4	68	9	AA826444	oe66a01.s	
C 555	12.8	44.1	77	13	BQ243044	BQ243044	TaE15019H	628	12.6	43.4	68	10	AW552311	L021D01-	
C 556	12.8	44.1	77	13	BQ244040	BQ244040	TaE15005F	629	12.6	43.4	68	29	CG730236	1119123D0	
C 557	12.8	44.1	77	14	CB562321	CB562321	66-B8867-	630	12.6	43.4	69	12	BG271713	na152f03.	
C 558	12.8	44.1	77	29	AG258132	AG258132	Lotus.cor	631	12.6	43.4	69	28	AZ818727	2M0088K22	
559	12.8	44.1	78	9	AA415410	AA415410	VD02f07.s	C 632	12.6	43.4	70	9	AI536249	vq99e07.x	
C 560	12.8	44.1	78	10	BG063280	BG063280	H305C03-	C 633	12.6	43.4	70	9	AI644963	vs48h01.y	
C 561	12.8	44.1	78	10	AW443383	AW443383	AB510.Pri	634	12.6	43.4	70	13	B0063954	Fgr.3.M18	
C 562	12.8	44.1	78	14	CD953730	CD953730	SBK_48.Gc	635	12.6	43.4	70	29	CG545898	OST143669	
C 563	12.8	44.1	78	14	CD953937	CD953937	SBM_106.G	636	12.6	43.4	71	28	AZ591297	IM0401014	
C 564	12.8	44.1	78	28	BZ379882	BZ379882	SALK_1141	637	12.6	43.4	72	10	AW173647	xj10d06.x	
C 565	12.8	44.1	78	29	CG473421	CG473421	OST858.Mu	638	12.6	43.4	72	12	BG793538	UTSW_SM13	
C 566	12.8	44.1	79	9	AI271934	AI271934	qj188f04.x	639	12.6	43.4	72	14	T25592	EST00628.Un	
C 567	12.8	44.1	79	29	CG604315	CG604315	OST279865	640	12.6	43.4	72	29	CG666004	OST455530	
C 568	12.8	44.1	79	29	AL760717	AL760717	Arabidops	C 641	12.6	43.4	73	10	BF400538	SMOVL3CAN	
569	12.8	44.1	80	13	BX783166	BX783166	EX783166	642	12.6	43.4	73	14	CB817159	d3a21p2.f	
C 570	12.8	44.1	80	29	CG574141	CG574141	OST206705	C 643	12.6	43.4	73	29	CG529491	OST109956	
C 571	12.6	43.4	25	28	AZ766828	AZ766828	IM0569C06	644	12.6	43.4	74	14	CD673927	fg05g01.x	
C 572	12.6	43.4	27	28	BZ379828	BZ379828	IM19074P0	645	12.6	43.4	74	14	CF651628	10-L02016	
C 573	12.6	43.4	29	28	BH866445	BH866445	SALK_1013	646	12.6	43.4	74	28	BZ556894	SALK_0897	
C 574	12.6	43.4	32	28	AZ929294	AZ929294	2M0277G18	647	12.6	43.4	74	29	CG597517	OST261044	
C 575	12.6	43.4	35	9	AU256066	AU256066	AU256066	C 648	12.6	43.4	75	9	AI254006	qv34d09.x	
576	12.6	43.4	35	9	AU252527	AU252527	AU252527	C 649	12.6	43.4	75	9	AI345051	tb01h03.x	
577	12.6	43.4	35	28	BH840522	BH840522	KG03386-5	C 650	12.6	43.4	75	9	AJ444040	AJ444040	
578	12.6	43.4	39	28	BX904511	BX904511	Arabidops	651	12.6	43.4	75	12	BM571633	fx04a07.x	
579	12.6	43.4	48	10	AW45085	AW45085	2819816.3	652	12.6	43.4	75	28	B46566	HS-1065-B1-	
C 581	12.6	43.4	50	9	AL779665	AL779665	AL779665	C 653	12.6	43.4	75	28	BZ382121	SALK_1178	
C 582	12.6	43.4	50	14	CF291606	CF291606	14ROOT--0	654	12.6	43.4	76	9	AI625418	ty54h12.x	
C 583	12.6	43.4	51	28	AZ582371	AZ582371	IM0374A17	655	12.6	43.4	76	13	BQ391463	NISC_mq18	
C 584	12.6	43.4	51	28	B01106	B01106	CSRL-125g12	656	12.6	43.4	76	14	CB817534	d311p2.f	
C 585	12.6	43.4	52	9	AA918429	AA918429	ol70h08.s	657	12.6	43.4	76	28	BZ288764	SALK_0221	
C 586	12.6	43.4	52	10	AW686481	AW686481	NF038E05N	C 658	12.6	43.4	77	9	AV847346	AV847346	
587	12.6	43.4	52	28	AZ308266	AZ308266	IM0011N04	659	12.6	43.4	77	10	AW246812	2822428.3	
588	12.6	43.4	52	28	B06941	B06941	CSRL-88F4-u	660	12.6	43.4	77	10	AW246812	2822428.3	
								661	12.6	43.4	77	14	CF013238	QBK3e08.x	

662	12.6	43.4	77	14	CF307808	ABF--01-F	C 735	12.4	42.8	61	29	CG513867	CG513867	Ost67472
C 663	12.6	43.4	77	28	A2480103	1M0301A22	C 736	12.4	42.8	62	29	BX892075	BX892075	ArabiDops
C 664	12.6	43.4	77	29	CG608441	Ost288586	C 737	12.4	42.8	63	29	AI271280	AI271280	QW83R01.X
C 665	12.6	43.4	77	29	CG608441	Ost288586	C 738	12.4	42.8	63	28	BX597224	BX597224	SALK_1005
C 666	12.6	43.4	78	9	AI494846	sb05b07.Y	C 739	12.4	42.8	64	9	AU053942	AU053942	AU053942
C 667	12.6	43.4	78	9	AI494846	sb05b07.Y	C 740	12.4	42.8	64	12	BI330183	BI330183	602983809
C 668	12.6	43.4	78	12	B07059307	B07059307	C 741	12.4	42.8	64	28	AZ433678	AZ433678	1M0219007
C 669	12.6	43.4	79	9	AA097644	mm36e12.X	C 742	12.4	42.8	64	29	AL751853	AL751853	ArabiDops
C 670	12.6	43.4	79	9	AA336213	nm36e12.X	C 743	12.4	42.8	65	9	AI281558	AI281558	QW52902.X
C 671	12.6	43.4	79	13	BQ582546	E012279-0	C 744	12.4	42.8	65	13	BX744236	BX744236	BX744236
C 672	12.6	43.4	79	28	CG041610	3591_114	C 745	12.4	42.8	65	29	CG662550	CG662550	Ost446737
C 673	12.6	43.4	79	29	AL951473	ArabiDops	C 746	12.4	42.8	66	28	AZ400381	AZ400381	1M0166G08
C 674	12.6	43.4	79	29	BX656286	ArabiDops	C 747	12.4	42.8	66	28	AZ492869	AZ492869	1M0227B13
C 675	12.6	43.4	80	14	CF313886	HD--10-J0	C 748	12.4	42.8	66	29	CG584009	CG584009	Ost226784
C 676	12.6	43.4	80	14	CF331598	NACL--07-	C 749	12.4	42.8	66	29	CG696248	CG696248	BARC_BFGL
C 677	12.6	43.4	80	14	CF331599	NACL--07-	C 750	12.4	42.8	66	29	CG696248	CG696248	BARC_BFGL
C 678	12.6	43.4	80	29	CG611871	OSP11817	C 751	12.4	42.8	67	9	AA894821	AA894821	Oj61d12.S
C 679	12.6	43.4	82	13	BX565934	SX565934	C 752	12.4	42.8	67	9	AA916806	AA916806	Q311002.S
C 680	12.4	42.8	24	20	AA248971	2819552.3	C 753	12.4	42.8	67	9	AI608823	AI608823	tw21104.X
C 681	12.4	42.8	24	28	BH790181	SALK_0565	C 754	12.4	42.8	67	14	CB264506	CB264506	54--B01499
C 682	12.4	42.8	24	28	BH866184	SALK_0955	C 755	12.4	42.8	67	14	CB264506	CB264506	54--B01499
C 683	12.4	42.8	32	28	A2583239	1M0378K08	C 756	12.4	42.8	67	29	CG589070	CG589070	Ost240770
C 684	12.4	42.8	34	9	AI457371	tl73c05.X	C 757	12.4	42.8	67	29	CG620673	CG620673	Ost318050
C 685	12.4	42.8	34	28	BH846289	SALK_0071	C 758	12.4	42.8	68	9	AI111605	AI111605	uf03e04.X
C 686	12.4	42.8	35	10	A250894	2821328.3	C 759	12.4	42.8	68	13	BQ586079	BQ586079	E012394-0
C 687	12.4	42.8	39	29	CG796995	SALK_1443	C 760	12.4	42.8	68	29	BX293339	BX293339	ArabiDops
C 688	12.4	42.8	40	9	AI500577	tn93b02.X	C 761	12.4	42.8	69	12	BM026997	BM026997	GIT0000086
C 689	12.4	42.8	42	29	CG869720	X0280 Sa	C 762	12.4	42.8	69	29	CG504738	CG504738	Ost53105
C 690	12.4	42.8	43	9	AI765730	w183g12.X	C 763	12.4	42.8	69	29	CG520443	CG520443	Ost85782
C 691	12.4	42.8	43	28	A2343822	1M0076K19	C 764	12.4	42.8	69	29	CG580218	CG580218	Ost219429
C 692	12.4	42.8	44	10	BX531819	602072738	C 765	12.4	42.8	70	9	AA931825	AA931825	om83a06.S
C 693	12.4	42.8	44	10	A250235	2822649.3	C 766	12.4	42.8	70	9	AI690994	AI690994	tl31b12.X
C 694	12.4	42.8	46	29	TA2190HP	AI79409 T. brucei	C 767	12.4	42.8	70	14	W20330	W20330	zb44d01.X
C 695	12.4	42.8	47	10	A250812	2822529.3	C 768	12.4	42.8	70	28	AZ049151	AZ049151	SSBRu1055
C 696	12.4	42.8	48	12	BJ048213	BJ048213	C 769	12.4	42.8	71	12	BI790370	BI790370	1d05904.X
C 697	12.4	42.8	48	10	A2343086	S30C3 AGS	C 770	12.4	42.8	71	28	AZ769221	AZ769221	1M0569B11
C 698	12.4	42.8	49	14	CF321218	HD--12-G0	C 771	12.4	42.8	71	28	AZ833302	AZ833302	2M0115E08
C 699	12.4	42.8	50	10	D19180	MUSGS00493	C 772	12.4	42.8	71	28	BH906047	BH906047	SALK_1091
C 700	12.4	42.8	50	10	A249795	2819793.3	C 773	12.4	42.8	71	28	BH906052	BH906052	SALK_1091
C 701	12.4	42.8	51	9	AA432731	vd72h09.X	C 774	12.4	42.8	72	28	BH851808	BH851808	1M0553F22
C 702	12.4	42.8	51	14	CG682301	rj49d02.Y	C 775	12.4	42.8	72	28	BH851808	BH851808	1M0553F22
C 703	12.4	42.8	52	9	AI697308	AI697308	C 776	12.4	42.8	72	28	BX597590	BX597590	SALK_1099
C 704	12.4	42.8	52	9	AU258888	AU258888	C 777	12.4	42.8	72	29	BX534001	BX534001	ArabiDops
C 705	12.4	42.8	52	10	BF637245	NF002F08L	C 778	12.4	42.8	73	9	AI665817	AI665817	AL965817
C 706	12.4	42.8	52	14	CG682289	rj49b06.Y	C 779	12.4	42.8	73	10	BF123392	BF123392	601759189
C 707	12.4	42.8	53	10	AM868435	NF038A01N	C 780	12.4	42.8	73	12	BG621583	BG621583	602617180
C 708	12.4	42.8	53	13	BX562212	BX562212	C 781	12.4	42.8	73	28	AZ797140	AZ797140	2M0053M10
C 709	12.4	42.8	53	28	A2467391	1M0278E18	C 782	12.4	42.8	74	9	AL652990	AL652990	AL652990
C 710	12.4	42.8	54	12	BG222772	nah38e10.	C 783	12.4	42.8	74	12	BG272589	BG272589	nah28b09.X
C 711	12.4	42.8	54	14	CF099569	rd86d06.Y	C 784	12.4	42.8	74	28	AZ479323	AZ479323	1M0299E22
C 712	12.4	42.8	55	9	AI913058	tz75f07.X	C 785	12.4	42.8	74	28	AZ9866310	AZ9866310	2M0268024
C 713	12.4	42.8	55	9	AI913453	tz77e09.X	C 786	12.4	42.8	74	29	CG560534	CG560534	Ost181152
C 714	12.4	42.8	55	9	AA555791	v155f01.X	C 787	12.4	42.8	75	9	AA615120	AA615120	vm02b09.X
C 715	12.4	42.8	55	29	AL938872	ArabiDops	C 788	12.4	42.8	75	13	BX736571	BX736571	EX736571
C 716	12.4	42.8	55	29	CG207713	Danio rer	C 789	12.4	42.8	75	13	BX736571	BX736571	EX736571
C 717	12.4	42.8	56	12	BM445434	1M11C9.a	C 790	12.4	42.8	75	29	BX897572	BX897572	1M0233H11
C 718	12.4	42.8	56	13	B0787611	1M13b12.X	C 791	12.4	42.8	75	29	CG597572	CG597572	ArabiDops
C 719	12.4	42.8	56	14	CG683163	CG683163	C 792	12.4	42.8	75	29	CNS01561	CNS01561	AL105043
C 720	12.4	42.8	56	28	B03759	CSRL-186F4-	C 793	12.4	42.8	76	10	AW396272	AW396272	2821685.3
C 721	12.4	42.8	56	29	AL943575	ArabiDops	C 794	12.4	42.8	76	10	AW396272	AW396272	2821685.3
C 722	12.4	42.8	57	12	BH873976	1a10C06.	C 795	12.4	42.8	76	13	BQ765474	BQ765474	EBR003.SQ
C 723	12.4	42.8	57	13	BX553132	BX553132	C 796	12.4	42.8	76	29	CG630076	CG630076	Ost344931
C 724	12.4	42.8	57	28	A2782127	2M0022B08	C 797	12.4	42.8	76	29	AI771944	AI771944	ArabiDops
C 725	12.4	42.8	58	9	AI052132	oy30c12.X	C 798	12.4	42.8	77	9	AI252082	AI252082	QW58b09.X
C 726	12.4	42.8	58	9	AI246109	q128h02.X	C 799	12.4	42.8	77	12	BI547556	BI547556	603236729
C 727	12.4	42.8	58	13	B0498406	pf5Steab9	C 800	12.4	42.8	77	12	BH846367	BH846367	SALK_0074
C 728	12.4	42.8	59	28	B2762290	SALK_0978	C 801	12.4	42.8	77	28	BZ358910	BZ358910	SALK_1335
C 729	12.4	42.8	60	9	AA931388	co03f09.S	C 802	12.4	42.8	77	28	BZ358910	BZ358910	SALK_1335
C 730	12.4	42.8	60	9	AI565932	tr95g11.X	C 803	12.4	42.8	77	29	CG551703	CG551703	Ost158956
C 731	12.4	42.8	60	9	AA161672	MBAFCG0E0	C 804	12.4	42.8	77	29	CG579050	CG579050	Ost316980
C 732	12.4	42.8	60	29	CG918490	1M0458-0	C 805	12.4	42.8	77	29	AL754972	AL754972	ArabiDops
C 733	12.4	42.8	61	14	R30999	Yb06e07.r1	C 806	12.4	42.8	78	9	AL593967	AL593967	AL593967
C 734	12.4	42.8	61	28	B04293	CSRL-2F11-u	C 807	12.4	42.8	79	9	AU259915	AU259915	Ost253889

C 808	12.4	42.8	79	10	AW395388	sh48d12.1.
C 809	12.4	42.8	79	12	B1703865	rm03a005.Y
C 910	12.4	42.8	79	14	CD682985	ij29a04.Y
C 811	12.4	42.8	79	29	AL948895	ArabiIdops
C 812	12.4	42.8	79	29	EX004713	ArabiIdops
C 813	12.4	42.8	80	10	BG021609	dg33b06.X
C 814	12.4	42.8	80	14	CF331113	NACL--07-
C 815	12.4	42.8	80	28	BH230335	1006157D0
C 816	12.2	42.1	20	28	AZ451921	1M0251C05
C 817	12.2	42.1	21	2	HSM001528	Homo sapi
C 818	12.2	42.1	25	2	HSM001707	Homo sapi
C 819	12.2	42.1	25	28	AZ851359	2M0153M02
C 820	12.2	42.1	26	28	AZ303394	1M0003J22
C 821	12.2	42.1	26	28	BZ664493	SALK_0756
C 822	12.2	42.1	27	28	BZ380070	SALK_1145
C 823	12.2	42.1	28	2	HSM001758	Homo sapi
C 824	12.2	42.1	28	2	HSM003578	Homo sapi
C 825	12.2	42.1	29	2	HSM001333	Homo sapi
C 826	12.2	42.1	29	2	HSM002271	Homo sapi
C 827	12.2	42.1	29	2	HSM002384	Homo sapi
C 828	12.2	42.1	29	2	HSM003053	Homo sapi
C 829	12.2	42.1	29	2	HSM003484	Homo sapi
C 830	12.2	42.1	29	2	AZ259463	AU259463
C 831	12.2	42.1	29	28	AZ345451	1M0808I12
C 832	12.2	42.1	30	2	HSM001432	Homo sapi
C 833	12.2	42.1	30	2	HSM001590	Homo sapi
C 834	12.2	42.1	30	2	HSM001698	Homo sapi
C 835	12.2	42.1	30	2	HSM002253	Homo sapi
C 836	12.2	42.1	30	2	HSM003231	Homo sapi
C 837	12.2	42.1	30	2	HSM003322	Homo sapi
C 838	12.2	42.1	30	2	HSM003483	Homo sapi
C 839	12.2	42.1	30	2	HSM003500	Homo sapi
C 840	12.2	42.1	30	9	AL048796	DKF2p566P
C 841	12.2	42.1	31	2	HSM002270	Homo sapi
C 842	12.2	42.1	31	2	HSM003327	Homo sapi
C 843	12.2	42.1	31	9	AA910955	OK67a10.1S
C 844	12.2	42.1	31	9	AA928444	cm77d06.1S
C 845	12.2	42.1	31	29	CG707293	111900I1H0
C 846	12.2	42.1	32	2	HSM001161	Homo sapi
C 847	12.2	42.1	32	2	HSM002171	Homo sapi
C 848	12.2	42.1	32	2	HSM002254	Homo sapi
C 849	12.2	42.1	32	9	AL036826	DKF2p564M
C 850	12.2	42.1	33	2	HSM001190	Homo sapi
C 851	12.2	42.1	33	2	HSM001806	Homo sapi
C 852	12.2	42.1	33	28	AZ316652	1M0034E23
C 853	12.2	42.1	35	2	HSM001908	Homo sapi
C 854	12.2	42.1	35	28	AZ819702	2M0091A01
C 855	12.2	42.1	36	2	HSM003463	Homo sapi
C 856	12.2	42.1	36	9	AZ254829	602666730
C 857	12.2	42.1	38	125	BG778513	602666730
C 858	12.2	42.1	38	28	AZ859079	2M0164I04
C 859	12.2	42.1	39	9	AU255393	AU255393
C 860	12.2	42.1	39	14	H55495	CHR220434.C
C 861	12.2	42.1	40	2	HSM003149	Homo sapi
C 862	12.2	42.1	40	9	AA878877	CF88g09.1S
C 863	12.2	42.1	41	2	HSM001284	Homo sapi
C 864	12.2	42.1	41	2	HSM002441	Homo sapi
C 865	12.2	42.1	41	12	B1388661	EST-CD34N
C 866	12.2	42.1	41	28	AZ837407	2M0132I09
C 867	12.2	42.1	41	28	BH861332	SALK_0580
C 868	12.2	42.1	43	2	HSM003157	Homo sapi
C 869	12.2	42.1	44	9	AW059908	ARUTH.bs
C 870	12.2	42.1	46	2	HSM001086	Homo sapi
C 871	12.2	42.1	46	2	HSM002006	Homo sapi
C 872	12.2	42.1	46	9	AA714376	tw20B06.1S
C 873	12.2	42.1	47	9	AU268330	AU268330
C 874	12.2	42.1	49	2	HSM001347	Homo sapi
C 875	12.2	42.1	49	2	HSM003587	Homo sapi
C 876	12.2	42.1	50	2	HSM002079	Homo sapi
C 877	12.2	42.1	50	9	AU104387	AU104387
C 878	12.2	42.1	50	13	BQ479308	BQ479308
C 879	12.2	42.1	50	13	EX002279	ArabiIdops
C 880	12.2	42.1	51	13	BQ584541	BQ584541

51	29	TA363H06P	AL494302	T. brucei
52	9	AU254794	AL756630	Arabidopsis
52	29	AU254794	AL756630	Arabidopsis
52	29	AU254794	AL756630	Arabidopsis
53	14	CA337586	NISC_1W03	CA337586 NISC_1W03
53	28	AZ780230	2M0017H1.9	AZ780230 2M0017H1.9
54	2	HSK001856	homo sapi	AL1037525 Homo sapi
54	9	AV832442	AV832442	AV832442 AV832442
54	9	AV832442	AV832442	AV832442 AV832442
54	14	CF929488	lagar7909	CF929488 lagar7909
54	14	CF929488	lagar7909	CF929488 lagar7909
54	29	CC556861	CH240_464	CC556861 CH240_464
54	29	CC556861	CH240_464	CC556861 CH240_464
54	29	TA185B03Q	AL473770	T. brucei
54	29	TA185B03Q	AL473770	T. brucei
55	2	HSN002268	AL1037934	Homo sapi
55	5	AL191537	AL191537	ge49b07.x
55	9	AL191537	AL191537	ge49b07.x
55	14	CF545724	CF545724	lad99f07.
55	14	CF545724	CF545724	lad99f07.
55	28	BA5176	BA5176	HS-1060-B2-
55	28	BA5176	BA5176	HS-1060-B2-
56	2	HSN001384	AL1037059	Homo sapi
56	2	HSN001384	AL1037059	Homo sapi
56	2	HSN002224	AL1037891	Homo sapi
56	9	A1251697	A1251697	gw45f01.x
56	9	A1251697	A1251697	gw45f01.x
56	28	B03428	B03428	CSRL-179A8-
57	10	BE302340	BE302340	bb48h03.x
57	28	AZ992314	AZ992314	2M0776K23
57	28	AZ992314	AZ992314	2M0776K23
57	28	BZ383549	BZ383549	SALK_1340
57	28	BZ383549	BZ383549	SALK_1340
57	28	CC038329	CC038329	359i_1_93
58	9	A1339339	A1339339	qt01h12.x
58	10	BF779328	BF779328	3173-48 h
58	10	BF779328	BF779328	3173-48 h
58	10	AW333702	AW333702	S25A3_AGS
58	14	CA850023	CA850023	k118e09.y
58	14	CA850023	CA850023	k118e09.y
58	28	AZ499503	AZ499503	1M0337M13
58	28	AZ499503	AZ499503	1M0337M13
58	29	CC936253	CC936253	lem5088_1
58	29	CC936253	CC936253	lem5088_1
59	9	A1251251	A1251251	qt55R06.x
59	14	CF801181	CF801181	rj35906.y
59	14	CF801181	CF801181	rj35906.y
60	9	A1251592	A1251592	gw45c12.x
60	9	A1251592	A1251592	gw45c12.x
60	10	BE317271	BE317271	NF058C01L
60	14	CF544876	CF544876	lad484ml
60	14	CF544876	CF544876	lad484ml
60	14	D20632	D20632	HUMG01607
60	14	D20632	D20632	HUMG01607
60	29	BX291566	BX291566	Arabidops
60	29	BX291566	BX291566	Arabidops
61	9	A1254437	A1254437	qt34dl1.x
61	9	A1254437	A1254437	qt34dl1.x
61	9	A1572940	A1572940	tn64B04.x
61	9	A1572940	A1572940	tn64B04.x
61	9	A1759171	A1759171	No.26 pol
61	12	BG944623	BG944623	ax53G04.x
61	12	BG944623	BG944623	ax53G04.x
61	14	CB165846	CB165846	RKT603019
61	14	CB165846	CB165846	RKT603019
61	14	N23759	N23759	yx80b11.sl
61	18	A2305244	A2305244	1M0005017
61	28	A2305244	A2305244	1M0005017
61	29	CG552817	CG552817	OST164248
61	29	CG552817	CG552817	OST164248
61	29	CG609348	CG609348	OST290484
61	29	CG609348	CG609348	OST290484
61	29	CG613243	CG613243	OST300251
61	29	CG613243	CG613243	OST300251
61	29	CG648205	CG648205	OST401092
61	29	CG648205	CG648205	OST401092
61	29	CG648935	CG648935	OST403356
61	29	CG648935	CG648935	OST403356
61	29	CG649884	CG649884	OST405666
61	29	CG649884	CG649884	OST405666
61	29	CG651118	CG651118	OST411531
61	29	CG651118	CG651118	OST411531
61	29	CG659726	CG659726	OST438216
61	29	CG659726	CG659726	OST438216
61	29	CG659725	CG659725	OST448667
61	29	CG659725	CG659725	OST448667
61	29	CG664520	CG664520	OST451893
61	29	CG664520	CG664520	OST451893
61	29	CG664529	CG664529	OST451912
61	29	CG664529	CG664529	OST451912
61	29	CG6656326	CG6656326	OST456260
61	29	CG6656326	CG6656326	OST456260
61	29	CG511479	CG511479	OST63864
62	29	CG511479	CG511479	OST63864
62	29	CG511584	CG511584	OST73448
62	29	CG511584	CG511584	OST73448
62	29	CG564371	CG564371	OST188428
62	29	CG564371	CG564371	OST188428
62	29	CG633433	CG633433	OST353081
62	29	CG633433	CG633433	OST353081
63	9	A1337629	A1337629	qwa6b04.x
63	9	A1337629	A1337629	qwa6b04.x
63	9	A1360526	A1360526	gx58e03.x
63	14	CA850289	CA850289	k126C02.y
63	14	CA850289	CA850289	k126C02.y
63	14	CD409013	CD409013	Gm. ck43577
63	14	CD409013	CD409013	Gm. ck43577
63	14	CD411244	CD411244	Gm. ck4051
63	14	CD411244	CD411244	Gm. ck4051
63	29	CG515616	CG515616	OST71849
63	29	CG515616	CG515616	OST71849
63	29	CG615571	CG615571	OST706351
63	29	CG615571	CG615571	OST706351
63	29	BX004050	BX004050	Arabidops
63	29	BX004050	BX004050	Arabidops
63	29	BX533881	BX533881	Arabidops
63	29	BX533881	BX533881	Arabidops
64	2	HSN002423	AL1038084	Homo sapi
64	2	HSN002423	AL1038084	Homo sapi
64	9	AA1815034	AA1815034	oa88b12.s
64	9	AA1815034	AA1815034	oa88b12.s
64	9	A1250459	A1250459	qx25h10.x
64	9	A1250459	A1250459	qx25h10.x
64	9	A12711399	A12711399	qw82e01.x
64	9	A12711399	A12711399	qw82e01.x
64	9	A1305424	A1305424	qw77a04.x
64	9	A1305424	A1305424	qw77a04.x
64	9	A1424361	A1424361	re59h05.x
64	9	A1424361	A1424361	re59h05.x

COMMENT					
Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:522107 Trace considered overall poor quality Possible reversed clone; similarity on wrong strand High quality sequence stop: 1.					
FEATURES					
source					
Location/Qualifiers					
1..70					
/organism="Mus musculus"					
/mol_type="mRNA"					
/strain="C57BL/6J x DBA/2J F1"					
/db_xref="taxon:10090"					
/clone="IMAGE:894147"					
/dev_stage="embryo"					
/lab_host="DH10B"					
/clone_lib="Knowles Solter mouse embryonic stem cell"					
/notes="Vector: pSPORT; Site 1: NotI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dnr) 5'-CGGTCGACCTGCACCGTGTATTTTTTT-3'. cDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies)."					
ORIGIN					
Query Match 63.4%; Score 18.4; DB 9; Length 70;					
Best Local Similarity 57.1%; Pred. No. 1.3e+04;					
Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;					
QY					
1 AAGAUUUUUUGAAGGCCCAAGGGC 28					
:::					
DB					
47 ACAGATCTCTTAGAACACCAGGGC 20					
RESULT 2					
AA708911/c					
LOCUS					
DEFINITION					
Z1644010.1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:506862.3, similar to SW:RB32_HUMAN Q13637 RAS-RELATED PROTEIN					
RAS-32 j; mRNA sequence.					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Homo sapiens (human)					
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE					
AUTHORS					
1 (bases 1 to 67) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R. WashU-NCI Human EST Project Unpublished (1997)					
TITLE					
JOURNAL					
COMMENT					
Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone; similarity on wrong strand Seq primer: -40mi3 fwd. Er from Amer sham High quality sequence stop: 1.					
FEATURES					
source					
Location/Qualifiers					
1..67					

C 954	12.2	42.1	64	9	A1583099	
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C 958	12.2	42.1	64	14	CF776307	
C 959	12.2	42.1	64	28	BH903232	
C 960	12.2	42.1	64	29	CG560851	
C 961	12.2	42.1	64	29	EX291457	
C 962	12.2	42.1	65	9	AL884705	
C 963	12.2	42.1	65	9	AU053940	
C 964	12.2	42.1	65	9	AV557638	
C 965	12.2	42.1	65	14	CF045820	
C 966	12.2	42.1	65	29	CNS03K4G	
C 967	12.2	42.1	66	9	AI571487	
C 968	12.2	42.1	66	9	AL698170	
C 969	12.2	42.1	66	12	BJ046023	
C 970	12.2	42.1	66	14	CB857842	
C 971	12.2	42.1	66	28	AZ471060	
C 972	12.2	42.1	66	28	AZ636071	
C 973	12.2	42.1	66	28	BH904509	
C 974	12.2	42.1	66	28	BH904510	
C 975	12.2	42.1	66	28	BZ663467	
C 976	12.2	42.1	66	29	AI762061	
C 977	12.2	42.1	67	9	AI423889	
C 978	12.2	42.1	67	9	AI798755	
C 979	12.2	42.1	67	14	CA334775	
C 980	12.2	42.1	67	14	CA335215	
C 981	12.2	42.1	67	29	BX004510	
C 982	12.2	42.1	67	29	T19BH08Q	
C 983	12.2	42.1	68	9	AI348734	
C 984	12.2	42.1	68	9	AA551800	
C 985	12.2	42.1	68	14	CB261164	
C 986	12.2	42.1	68	14	CB353381	
C 987	12.2	42.1	68	28	AZ779515	
C 988	12.2	42.1	68	28	BZ288968	
C 989	12.2	42.1	68	29	CG547926	
C 990	12.2	42.1	69	12	BG944637	
C 991	12.2	42.1	69	12	BW023345	
C 992	12.2	42.1	69	14	CA335433	
C 993	12.2	42.1	69	14	CD712860	
C 994	12.2	42.1	69	14	CP922033	
C 995	12.2	42.1	69	28	AZ599420	
C 996	12.2	42.1	69	29	CG516082	
C 997	12.2	42.1	69	29	CG530939	
C 998	12.2	42.1	70	9	AI308361	
C 999	12.2	42.1	70	9	A1337559	
C 1000	12.2	42.1	70	9	A1337559	

RESULT 1
 Locus AAS16989/c
 DEFINITION vhs9d02.r1 Knowles Solter mouse embryonic stem cell Mus musculus cDNA clone IMAGE:894147 5' similar to TR:G187568 G187568 MG44 ; mRNA sequence.

(ACCESSION AAS16989
 VERSION AA516989.1 GI:22556448
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus)

REFERENCE
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B., Schellenberg,K., Steproe,M., Tan,F., Underwood,K., Moore,B., Thaising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston R.

TITLE The WashU-HMMI Mouse EST Project

ALIGNMENTS

70 bp mRNA linear EST 14-JUL-1997

vhs9d02.r1 Knowles Solter mouse embryonic stem cell Mus musculus cDNA clone IMAGE:894147 5' similar to TR:G187568 G187568 MG44 ; , mRNA sequence.

```

AAS16989          70 bp      mRNA       linear   EST 14-JUL-1997
vhs9d02.r1        Knowles Solter mouse embryonic stem cell Mus musculus
cDNA clone IMAGE:894147 5' similar to TR:G187568 G187568 MG44 ; ,
mRNA sequence.
AA516989
AA516989.1        GI:22556448
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 70)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B.,
Schellenberg,K., Steproe,M., Tan,F., Underwood,K., Moore,B.,
Thaising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston R.
The WashU-HMMI Mouse EST Project
```

C	954
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C	988
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C	992
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C	994
C	995
C	996
C	997
C	998
C	999
C	1000

RESULT 1
AA516989/c
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE.


```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3812701"
/db_xref="taxon:9606"
/clone="IMAGE:506682"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/notes="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGATTTCGGCGCGCTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

```

ORIGIN

```

Query Match          60.0%; Score 17.4; DB 9; Length 67;
Best Local Similarity 55.8%; Pred. No. 3e+04; 6; Indels 0; Gaps 0;
Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 3 AGAUCUUUUUUAAGCCCAAGGCU 29
DB 51 AGAGACTTCTGTAAACCCCAAGGCT 25

```

RESULT 3

```

AI609394/c
LOCUS              70 bp mRNA linear EST 16-DEC-1999
DEFINITION          tw93503.x1 NCI_CGAP_HN6 Homo sapiens cDNA clone IMAGE:2267213 3' similar to SW:TCFH_HUMAN Q99832 T-COMPLEX PROTEIN 1, ETA SUBUNIT ;, mRNA sequence.
ACCESSION            AI609394
VERSION              AI609394.1 GI:4618561
KEYWORDS              EST.
SOURCE                Homo sapiens (human)
ORGANISM              Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 70)
NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
JOURNAL
COMMENT              Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Chong Heon Lee, D.D.S., Mary May, J. Silvio Gutkind, Ph.D., Myung Hee Park, Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

```

```

Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Chong Heon Lee, D.D.S., Mary May, J. Silvio Gutkind, Ph.D., Myung Hee Park, Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

```

```

Trace considered overall poor quality
Insert Length: 2028 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

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FEATURES

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Source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2267213"
/tissue_types="normal gingiva (cell line from immortalized keratinocytes)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI_CGAP_HN6"

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/notes="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. 5' adaptor sequence: 5' AATTCGCGACGAG 3', GCGGTC 5' 3' adaptor sequence: 5' (GA)10ACTAGTCGAGTTT 3', EcoRI site appears to have been lost in a fraction of the clones. Library constructed by Stratagene; available through Mary May, PhD (Oral and Pharyngeal Cancer Branch, National Institute of Dental and Craniofacial Research, NIH; mmay@odonid.nih.gov)."

```

ORIGIN

```

Query Match          57.2%; Score 16.6; DB 9; Length 70;
Best Local Similarity 47.8%; Pred. No. 5.9e+04;
Matches 11; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 6 UCUUUUUUUAAGCCCAAGGCU 28
DB 54 TTTTGTGTGGGCCCCAAGGCC 32

```

RESULT 4

```

H07686/c
LOCUS              75 bp mRNA linear EST 23-JUN-1995
DEFINITION          Khs012 BNL1 Brassica napus cDNA 3', mRNA sequence.
ACCESSION            H07686
VERSION              H07686.1 GI:872508
KEYWORDS              EST.
SOURCE                Brassica napus (rape)
ORGANISM              Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 75)
Sohn,U., Lee,C.M., Cho,K.H., Jeon,Y.H., Hahn,T.R. and Nam,H.G.
cDNAs from Brassica napus (rape)
Unpublished (1995)
Contact: Uik Sohn
Laboratory of Molecular Biology
Kyungpook National University
Dept. of Genetic Eng., Kyungpook National Univ., Taegu 702-701, Korea
Tel: 0539505382
Fax: 0539555327
Email: usohn@bh.kyungpook.ac.kr
EST is putatively homologous to unknown gene
Seq primer: M13 forward.

```

FEATURES

```

Source
1..75
/organism="Brassica napus"
/mol_type="mRNA"
/strain="cv. Naehan"
/db_xref="taxon:3708"
/lab_host="NMS22"
/clone_lib="BNL1"
/notes="Vector: pT7T3D; Site 1: NotI; Site 2: EcoRI; Poly(A)-mRNA was purified from the leaf of B.napus. cDNA library was constructed from the mRNAs by oligo(dT) priming and directionally cloned from the NotI site in the vector pT7T3D (Pharmacia) to the EcoRI site."

```

ORIGIN

```

Query Match          57.2%; Score 16.6; DB 14; Length 75;
Best Local Similarity 56.5%; Pred. No. 5.9e+04;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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QY 7 UCUUUUUUUAAGCCCAAGGCU 29
DB 34 TCTTCTTGAAGCTCCCAAGGCT 12

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RESULT 5

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BG361927/c
LOCUS              51 bp mRNA linear EST 08-MAR-2001

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DEFINITION gb49d10.y1 Moss EST library PPG Physcomitrella patens cDNA clone
 PEP_SOURCE_ID: 5', mRNA sequence.
 ACCESSION BG361927
 VERSION BG361927.1 GI:13251024
 KEYWORDS EST.
 SOURCE Physcomitrella patens
 ORGANISM Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
 1 (Bases 1 to 51)
 REFERENCE Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,
 Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
 Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
 Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
 Leeds/Wash U Moss EST Project
 Unpublished (1999)
 TITLE Contact: Ralph Quatrano
 JOURNAL Leeds/Wash U Moss EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..51
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE ID:"
 /tissue_type="gametophore: 30 day old tissue,
 ammonium-grown"
 /lab_host="DH10B"
 /clone_lib="Moss EST library PPG"
 /note="Vector: pAMP1; Construction of the cDNA library was
 performed by Dr. W. Gregg Clark using a modification of
 the cDNA synthesis protocol developed in the laboratory of
 Dr. Michael Lovett by Dr. Yulia Korshunova (personal
 communication). First polyA + RNA was isolated from total
 gametophore RNA using oligo dT magnetic beads. Following
 this, first strand cDNA synthesis was performed on the
 bead-bound polyA + RNA, during which an oligonucleotide
 anchor sequence was incorporated onto the 5'-ends of the
 cDNA. PCR amplification was then used to synthesize the
 second strand to amplify the double stranded DNA, and to
 incorporate dUTP containing sequences into the ends of the
 double stranded cDNA. This DNA was size selected and
 cloned into pAMP1 using the CloneAMP pAMP1 System (Life
 Technologies, GibcoBRL) for cloning amplification products
 by a non-restriction site dependant process. The cloning
 was directional based on sequence asymmetry introduced at
 the ends during PCR amplification. The 3' cDNA ends are
 proximal to the NotI site of the multiple cloning site in
 pAMP1. This annealing mixture was transformed into
 chemically competent DH10B cells and selected for
 ampicillin resistant growth. The resulting clones (about
 330,000) were pooled to make the library."

ORIGIN

Query Match 55.2%; Score 16; DB 12; Length 51;
 Best Local Similarity 41.7%; Pred. No. 1.1e+05;
 Matches 10; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 6 UUCUUUUGAAGCCCAAGGCU 29
 :: ::::: ||||| |:
 Db 27 TTTTITTTTAAAGCCCAAGACT 4

RESULT 6
 BG361878/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BG361878 73 bp mRNA linear EST 08-MAR-2001
 gb46b10.y1 Moss EST library PPG Physcomitrella patens cDNA clone
 PEP_SOURCE_ID: 5', mRNA sequence.
 ACCESSION BG361878
 VERSION BG361878.1 GI:13250975
 KEYWORDS EST.
 SOURCE Physcomitrella patens
 ORGANISM Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
 1 (Bases 1 to 73)
 REFERENCE Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,
 Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
 Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
 Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
 Leeds/Wash U Moss EST Project
 Unpublished (1999)
 TITLE Contact: Ralph Quatrano
 JOURNAL Leeds/Wash U Moss EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..73
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE ID:"
 /tissue_type="gametophore: 30 day old tissue,
 ammonium-grown"
 /lab_host="DH10B"
 /clone_lib="Moss EST library PPG"
 /note="Vector: pAMP1; Construction of the cDNA library was
 performed by Dr. W. Gregg Clark using a modification of
 the cDNA synthesis protocol developed in the laboratory of
 Dr. Michael Lovett by Dr. Yulia Korshunova (personal
 communication). First polyA + RNA was isolated from total
 gametophore RNA using oligo dT magnetic beads. Following
 this, first strand cDNA synthesis was performed on the
 bead-bound polyA + RNA, during which an oligonucleotide
 anchor sequence was incorporated onto the 5'-ends of the
 cDNA. PCR amplification was then used to synthesize the
 second strand to amplify the double stranded DNA, and to
 incorporate dUTP containing sequences into the ends of the
 double stranded cDNA. This DNA was size selected and
 cloned into pAMP1 using the CloneAMP pAMP1 System (Life
 Technologies, GibcoBRL) for cloning amplification products
 by a non-restriction site dependant process. The cloning
 was directional based on sequence asymmetry introduced at
 the ends during PCR amplification. The 3' cDNA ends are
 proximal to the NotI site of the multiple cloning site in
 pAMP1. This annealing mixture was transformed into
 chemically competent DH10B cells and selected for
 ampicillin resistant growth. The resulting clones (about
 330,000) were pooled to make the library."

FEATURES
 source

1..73
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE ID:"
 /tissue_type="gametophore: 30 day old tissue,
 ammonium-grown"
 /lab_host="DH10B"
 /clone_lib="Moss EST library PPG"
 /note="Vector: pAMP1; Construction of the cDNA library was
 performed by Dr. W. Gregg Clark using a modification of
 the cDNA synthesis protocol developed in the laboratory of
 Dr. Michael Lovett by Dr. Yulia Korshunova (personal
 communication). First polyA + RNA was isolated from total
 gametophore RNA using oligo dT magnetic beads. Following
 this, first strand cDNA synthesis was performed on the
 bead-bound polyA + RNA, during which an oligonucleotide
 anchor sequence was incorporated onto the 5'-ends of the
 cDNA. PCR amplification was then used to synthesize the
 second strand to amplify the double stranded DNA, and to
 incorporate dUTP containing sequences into the ends of the
 double stranded cDNA. This DNA was size selected and
 cloned into pAMP1 using the CloneAMP pAMP1 System (Life
 Technologies, GibcoBRL) for cloning amplification products
 by a non-restriction site dependant process. The cloning
 was directional based on sequence asymmetry introduced at
 the ends during PCR amplification. The 3' cDNA ends are
 proximal to the NotI site of the multiple cloning site in
 pAMP1. This annealing mixture was transformed into
 chemically competent DH10B cells and selected for
 ampicillin resistant growth. The resulting clones (about
 330,000) were pooled to make the library."

ORIGIN

Query Match 55.2%; Score 16; DB 12; Length 73;
 Best Local Similarity 45.8%; Pred. No. 9.9e+04;
 Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

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Qy 6 UUUUUUUUUAAGCCCAAGGCU 29
Db 40 TTTTGGGAGCCCAAGACT 17

RESULT 7
AI824019/c
LOCUS
DEFINITION
  wj29f03.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2404253 3'
  similar to TR:070278 070278 MULTIPLE ENDOCRINE NEOPLASIA TYPE 1
  CANDIDATE PROTEIN NUMBER 18. ;, mRNA sequence.
ACCESSION
  AI824019
VERSION
  AI824019.1 GI:5444690
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 58)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 806 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
  source
  1..58
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:2404253"
  /tissue_type="2 pooled tumors (clear cell type)"
  /lab_host="DH10B"
  /clone_lib="NCI CGAP Kid12"
  /note="Organ: kidney; Vector: pTT73D-pac (Pharmacia) with
  a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
  Plasmid DNA from the normalized library NCI CGAP Kids was
  prepared, and ss circles were made in vitro. Following HAP
  purification, this DNA was used as tracer in a subtractive
  hybridization reaction. The driver was PCR-amplified cDNAs
  from a pool of 5,000 clones made from the same library
  (clones IDs 1323912-1325831, 1471368-1472903 and
  1492104-1493255). Subtraction by Bento Soares and M.
  Fatima Bonaldo."

ORIGIN
  Query Match 54.5%; Score 15.8; DB 9; Length 58;
  Best Local Similarity 44.4%; Pred. No. 1.2e+05;
  Matches 12; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGAUUUUUUUUAAGCCCAAGGCU 29
Db 56 AGCTTTTTCCTCAAGTCCCAAGAGCT 30

RESULT 8
BQ613481/c
LOCUS
DEFINITION
  BQ613481
  rd07h06.y1 Meloidogyne incognita egg SL1 TOPO VI Meloidogyne
  incognita cDNA 5', mRNA sequence.

ORIGIN
  Query Match 54.5%; Score 15.8; DB 9; Length 58;
  Best Local Similarity 44.4%; Pred. No. 1.2e+05;
  Matches 12; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 9 UUUUUUUUAAGCCCAAGGCU 27
Db 47 TTTTCTAAGCCCAAGGCGG 29

RESULT 9
AZ657549
LOCUS
DEFINITION
  AZ657549
  1M053318R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M053318 R, genomic survey sequence.
ACCESSION
  AZ657549
VERSION
  AZ657549.1 GI:11794695
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 76)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Famil, C.,
  Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

ACCESSION
  BQ613481
VERSION
  BQ613481.1 GI:21603157
KEYWORDS
  EST.
SOURCE
  Meloidogyne incognita (southern root-knot nematode)
  Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
  Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE
  1 (bases 1 to 72)
  McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
  Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
  Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
  Tsagaris, V., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
  Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
  Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
  McCann, R., Waterston, R. and Wilson, R.
  The Washington Univ. Nematode EST Project, 1999
  Unpublished (1999)
JOURNAL
  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  The library was constructed by Claire Murphy and Dr. James McCarter
  at Washington University, St. Louis. Meloidogyne incognita eggs
  were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.
  Putative full length read
  The vector to vector length is 73
  Seq primer: -40RP from Gibco.
  Location/Qualifiers
  1..72
  /organism="Meloidogyne incognita"
  /mol_type="mRNA"
  /db_xref="taxon:6306"
  /dev_stage="egg"
  /lab_host="DH10B (Invitrogen)"
  /clone_lib="Meloidogyne incognita egg SL1 TOPO v1"
  /note="Vector: pCR11-TOPO (Invitrogen); Site 1: EcoRI;
  Site 2: EcoRI; The library was constructed by Claire
  Murphy and Dr. James McCarter at Washington University,
  St. Louis. Oligo (dT)-SL1 PCR based library. cDNA PCR
  products of size >400 nucleotides containing SL1 on the 5'
  end and oligo(dT) on the 3' end were non-directionally
  cloned into pCR11-TOPO (Invitrogen) following the TOPO TA
  cloning protocol. Meloidogyne incognita eggs were provided
  by Andrew Kloek of Divergence Inc., St. Louis, MO."

ORIGIN
  Query Match 54.5%; Score 15.8; DB 13; Length 72;
  Best Local Similarity 57.9%; Pred. No. 1.2e+05;
  Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 9 UUUUUUUUAAGCCCAAGGCU 27
Db 47 TTTTCTAAGCCCAAGGCGG 29

RESULT 9
AZ657549
LOCUS
DEFINITION
  AZ657549
  1M053318R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M053318 R, genomic survey sequence.
ACCESSION
  AZ657549
VERSION
  AZ657549.1 GI:11794695
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 76)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Famil, C.,
  Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

```

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0533 row: L column: 18
 Seq primer: CACACAGAAACACGATGACC
 Class: plasmid ends
 High quality sequence stop: 76.
 Location/Qualifiers
 1. 76
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGC1M0533L18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G1/473114[GB|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 54.5%; Score 15.8; DB 28; Length 76;
 Best Local Similarity 44.4%; Pred. No. 1.2e+05;
 Matches 12; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGAUCUUUUUUAAGCCCAAGGCU 29
 |||:|||||:|||||:|||||:
 Db 43 AGTTCTTTTGGAGGCACTCAGACT 69
 |||:|||||:|||||:|||||:

RESULT 10
 A1802260 37 bp mRNA linear EST 13-DEC-1999
 t336907.x1 NCI CGAP Panel Homo sapiens cDNA clone IMAGE:2143644 3' similar to TR:Q41120 Q41120 HYDROXYPROLINE-RICH GLYCOPROTEIN ; mRNA sequence.

ACCESSION A1802260
 VERSION A1802260.1 GI:5367732
 LOCUS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 37)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabbs@mail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbr/image/image.html

Trace considered overall poor quality
 Insert Length: 1470 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2143644"
 /tissue_type="adenocarcinoma"
 /lab_host="NCI CGAP Panel"
 /clone_lib="NCI CGAP Panel"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN
 Query Match 53.8%; Score 15.6; DB 9; Length 37;
 Best Local Similarity 50.0%; Pred. No. 1.6e+05;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAGAUCUUUUUUAAGGCCCC 22
 |||:|||||:|||||:|||||:
 Db 7 AAAATTTTITTTTGGAGGCCCC 28
 |||:|||||:|||||:|||||:

RESULT 11
 A2834846/c 58 bp DNA linear GSS 20-FEB-2001
 2M0117F18R Mouse 10kb plasmid UGC1M library Mus musculus genomic clone UGC2M0117F18 R, genomic survey sequence.

ACCESSION A2834846
 VERSION A2834846.1 GI:13004754
 LOCUS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 58)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0117 row: F column: 18
 Seq primer: CACACAGAAACACGATGACC
 Class: plasmid ends
 High quality sequence stop: 58.
 Location/Qualifiers

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabbs@mail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbr/image/image.html

Trace considered overall poor quality
 Insert Length: 1470 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2143644"
 /tissue_type="adenocarcinoma"
 /lab_host="NCI CGAP Panel"
 /clone_lib="NCI CGAP Panel"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN
 Query Match 53.8%; Score 15.6; DB 9; Length 37;
 Best Local Similarity 50.0%; Pred. No. 1.6e+05;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAGAUCUUUUUUAAGGCCCC 22
 |||:|||||:|||||:|||||:
 Db 7 AAAATTTTITTTTGGAGGCCCC 28
 |||:|||||:|||||:|||||:

RESULT 11
 A2834846/c 58 bp DNA linear GSS 20-FEB-2001
 2M0117F18R Mouse 10kb plasmid UGC1M library Mus musculus genomic clone UGC2M0117F18 R, genomic survey sequence.

ACCESSION A2834846
 VERSION A2834846.1 GI:13004754
 LOCUS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 58)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0117 row: F column: 18
 Seq primer: CACACAGAAACACGATGACC
 Class: plasmid ends
 High quality sequence stop: 58.
 Location/Qualifiers

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source
1. 58
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0117F18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114[GB|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 53.8%; Score 15.6; DB 28; Length 58;
Best Local Similarity 54.5%; Pred. No. 1.4e+05;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAG 25
|::|::|::|::|::|::|
Db 24 GTTTCCTTTGTTATCCCAAG 3

RESULT 12
U44334 49 bp mRNA linear EST 03-APR-1996
LOCUS ENU44334 Aspergillus nidulans cleistothecium Emericella nidulans
DEFINITION cDNA clone SE0762, mRNA sequence.
ACCESSION U44334.1 GI:1244997
VERSION U44334
KEYWORDS Emericella nidulans (anamorph: Aspergillus nidulans)
SOURCE Emericella nidulans
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 49)
AUTHORS Lee,D., Lee,S., Hwang,H., Kim,J. and Chae,K.
TITLE Quantitative analysis of gene expression in sexual structures of Aspergillus nidulans by sequencing of 3'-directed cDNA clones
JOURNAL FEMS Microbiol. Lett. 138 (1), 71-76 (1996)
MEDLINE 96236220
PUBMED 8674973
COMMENT Contact: Keon-Sang Chae
Chonbuk National University
Chonju, 561-756, S. Korea
Tel: +82-652-70-3340
Fax: +82-652-70-3345
Email: chae@chonbuknms.chonbuk.ac.kr.

FEATURES
Location/Qualifiers
1. 49
/mol_type="mRNA"
/organism="Emericella nidulans"
/strain="FGSC4"
/db_xref="taxon:162425"
/clone="SE0762"
/tissue_type="cleistothecium"
/cell_type="Hull Cell"

source
/dev_stage="sexual"
/clone_lib="Aspergillus nidulans cleistothecium"
/notes="3'-directed cDNA clones; single-pass sequencing"

ORIGIN
Query Match 53.1%; Score 15.4; DB 28; Length 49;
Best Local Similarity 52.0%; Pred. No. 1.8e+05;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 AGAUUCUUUUUGUAGCCCAAGG 27
|::|::|::|::|::|::|
Db 20 AGATTCTTTCATTAACTCCCAAGG 44

RESULT 13
BH252676 77 bp DNA linear GSS 28-NOV-2001
LOCUS SALK_013733 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_013733, genomic survey sequence.
DEFINITION BH252676
ACCESSION BH252676.1 GI:17139654
VERSION BH252676
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 77)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 77
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_013733"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 53.1%; Score 15.4; DB 28; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.6e+05;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGAUCUUUUUGUAA 17
|::|::|::|::|::|::|
Db 9 AATGATTCCTTTTGTA 25

RESULT 14
AG260396 78 bp DNA linear GSS 22-JUL-2003
LOCUS Lotus corniculatus var. japonicus DNA, clone:LJT50h16_sfi, genomic
DEFINITION

```

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survey sequence.
ACCESSION AG260396
VERSION AG260396.1 GI:26660233
KEYWORDS GSS.
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM Lotus corniculatus var. japonicus
REFERENCE Sato, S., Nakamura, Y. and Tabata, S.
AUTHORS Lotus japonicus TAC End sequences
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 78)
AUTHORS Sato, S.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp; URL: http://www.kazusa.or.jp/en/plant/.
Tel: 81-438-52-3935 (ex.2336), Fax: 81-438-52-3934)
FEATURES
Location/Qualifiers
1..78
/molecule="DNA"
/organism="Lotus corniculatus var. japonicus"
/strain="Wakajima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjT50h16_sfi"
/clone_lib="genomic TAC library"
/note="VECTOR: pYL7AC7-synonym: Lotus japonicus"
ORIGIN
Query Match 53.1%; Score 15.4; DB 29; Length 78;
Best Local Similarity 58.8%; Pred. No. 1.6e+05;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 9 UUUUGUAGCCCAAG 25
Db 22 TTTTGTAGACCCCAAG 6
RESULT 15
AI318033
LOCUS
DEFINITION ta75902 x1 NCI CGAP HSC2 Homo sapiens cDNA clone IMAGE:2049938 3,
similar to SW-RL34_HUMAN P49207 60S RIBOSOMAL PROTEIN L34. ; mRNA
sequence.
ACCESSION AI318033
VERSION AI318033.1 GI:4033793
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 61)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 384 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..61
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2049938"
/tissue_type="stem cell 34+/38+"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP HSC2"
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from
bone marrow, stem cells 34+/38+, cDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 400 bp. Primary library,
non-amplified."
ORIGIN
Query Match 52.4%; Score 15.2; DB 9; Length 61;
Best Local Similarity 53.6%; Pred. No. 2e+05;
Matches 15; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 AAAGAUCUUUUUUAAGCCCAAGGCC 28
Db 1 AAGGGTTCGTGCTGTATGACCTAAGGCC 28
RESULT 16
BM517546
LOCUS
DEFINITION 'xj80g07.y1 Ascaris suum female head SL1 TOPO v1 Murphy Chiapelli
McCarter Ascaris suum cDNA 5', mRNA sequence.
ACCESSION BM517546
VERSION BM517546.1 GI:18688698
KEYWORDS EST.
SOURCE Ascaris suum (pig roundworm)
ORGANISM Ascaris suum
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
AUTHORS Ascaridoidea; Ascaridae; Ascaris.
1 (bases 1 to 65)
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, I., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarelashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter, J.P.
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Claire Murphy, Brandi Chiapelli, and
Dr. James McCarter at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center.
FEATURES
Location/Qualifiers
1..65
/organism="Ascaris suum"
/mol_type="mRNA"
/db_xref="taxon:6253"
/sex="female"
/tissue_type="Head"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Ascaris suum female head SL1 TOPO v1 Murphy
Chiapelli McCarter"
/note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;

```

Site 2: EcoRI; The library was constructed by Claire Murphy, Brandi Chiapelli, and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-S11 PCR based library. Ascaris sum female head cDNA PCR products of size >400 nucleotides containing S11 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(invitrogen) following the TOPO TA cloning protocol. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhsph.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD"

ORIGIN

Query Match 52.4%; Score 15.2; DB 12; Length 65;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AAGAUUUUUUUAAGCCCAAGGCGU 29

Db 1 AAGTTCTGTTTATGAGACCGAGATCT 28

RESULT 17
LOCUS AA936218/c
DEFINITION ON43C10.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1559442 3',
mRNA sequence.

ACCESSION AA936218

VERSION AA936218.1 GI:3094136

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 78)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 1346 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 52.

Location/Qualifiers

1..78

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1559442"

/tissue_type="adenocarcinoma"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_C08"

/note="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

colon adenocarcinoma, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified p7T3

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Donaldo."

ORIGIN

Query Match 52.4%; Score 15.2; DB 9; Length 78;

Best Local Similarity 46.4%; Pred. No. 1.9e+05;

Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 2 AAGAUUUUUUUAAGCCCAAGGCGU 29
Db 77 AGTTCTGTTTATGAGACCGACCCCT 50

RESULT 18
LOCUS B02943/c
DEFINITION B02943
ACCESSION B02943.1 GI:1412221
VERSION B02943.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 58)

Jones, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,

Evans, D., Ward, T., Gillilan, E., Schlegemann, J., Probst, S.,

Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M.,

Kupfer, K. and Garner, H.R.

Genomic Sequence Sampled Map of Chromosome 11

Unpublished (1996)

Contact: Evans GA, Shane Probst

McDermott Center for Human Growth and Development

University of Texas Southwestern Medical Center At Dallas

5323 Harry Hines Blvd, Dallas TX 75235-8591

Tel: 214-648-1600

Fax: 214-648-1666

Email: gevan@utsw.swmed.edu, shane@mcdermott.swmed.edu

Seq primer: T7

Class: cosmid ends

High quality sequence stop: 58.

Location/Qualifiers

1..58

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="CSRL-163G2"

/sex="female"

/cell_type="chimeric hamster somatic cell hybrid"

/clone_lib="CSRL flow sorted Chromosome 11 specific

cosmid"

/note="Vector: sCos-1; Human Chromosome 11 specific cosmid

library prepared from flow sorted human Chromosome 11

derived from Chinese Hamster Ovary (CHO) monochromosomal

somatic cell hybrid, J1"

ORIGIN

Query Match 51.7%; Score 15; DB 28; Length 58;

Best Local Similarity 43.5%; Pred. No. 2.4e+05;

Matches 10; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 6 UUUUUUUUAAGCCCAAGGCGC 28

Db 41 TTTTCTTTTGTATGATCCCAAGGCGC 19

RESULT 19
LOCUS CD682098/c
DEFINITION rj46C08.y1 Meloidogyne chitwoodi egg SL1 TOPO v1 Meloidogyne
chitwoodi cDNA 5', mRNA sequence.

ACCESSION CD682098

VERSION CD682098.1 GI:32183864

KEYWORDS EST.

SOURCE Meloidogyne chitwoodi

Meloidogyne chitwoodi

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

REFERENCE
AUTHORS

1 (bases 1 to 68)
McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagaris, V., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R., and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

TITLE
JOURNAL
COMMENT

Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

The library was constructed by Claire Murphy and Dr. Makedonka Dautova at Washington University, St. Louis (mdautova@watson.wustl.edu). Oligo(dT)-SL1 PCR based library. Meloidogyne chitwoodi egg cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally ally cloned into pCRII-TOPO (Invitrogen) following the TOPO TA cloning protocol. Eggs were provided by Dr. David Bird of North Carolina State University, Raleigh, NC (david.bird@ncsu.edu).

Putative full length read

The vector to vector length is 69

Seq primer: SL1 primer.

FEATURES
Source

Location/Qualifiers
1..68

/organism="Meloidogyne chitwoodi"
/mol_type="mRNA"
/db_xref="taxon:59747"
/dev_stage="eggs"
/lab_host="DH10B"
/clone_lib="Meloidogyne chitwoodi egg SL1 TOPO v1"
/note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI; Site 2: EcoRI; The library was constructed by Claire Murphy and Dr. Makedonka Dautova at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Meloidogyne chitwoodi egg cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO (Invitrogen) following the TOPO TA cloning protocol. Eggs were provided by Dr. David Bird of North Carolina State University, Raleigh, NC (david.bird@ncsu.edu)."

ORIGIN

Query Match 51.7%; Score 15; DB 14; Length 68;

Best Local Similarity 47.8%; Pred. No. 2.4e+05;

Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 6 UUUUUUUUUAAGCCCAAGGCGC 28

DB 57 TTCTCTTTTAAAGCCTCACCGCGC 35

RESULT 20
AZ840876/c

LOCUS 34 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0138C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0138C08 R, genomic survey sequence.

ACCESSION AZ840876

VERSION GI:13010784

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 34)

REFERENCE

1 (bases 1 to 34)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE
JOURNAL
COMMENT

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0138 row: C column: 08
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.

FEATURES
source

Location/Qualifiers
1..34

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0138C08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 14.8; DB 28; Length 34;

Best Local Similarity 57.7%; Pred. No. 3.2e+05;

Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 AGAUUCUUUUGUAGCCCAAGGCGC 28

DB 26 ATATAATCTTCGAAGCACCACCAAGGCGC 1

RESULT 21
AZ576537

LOCUS 49 bp DNA linear GSS 06-DEC-2000
DEFINITION AST-T11C0260\ (Genetrapp T47D Human Breast Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.

ACCESSION AZ576537

VERSION GI:11562848

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

REFERENCE

1 (bases 1 to 49)

Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M.,

Bernardino, A., Durick, K. and Pollok, B.


```

QY 4 GAUUCUUUUUGUAGCCCAAGCGGU 29
DB 15 GATTCTCTCTGTAGGCAATGTCT 40

RESULT 24
CG588850 67 bp DNA linear GSS 02-OCT-2003
OS1240321 Mus musculus 129Sv/Ev Mus musculus genomic clone
OS1240321, genomic survey sequence.
ACCESSION CG588850
VERSION CG588850
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 67)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W.Jr., Kipp,P., Kohlhaufl,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtehorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
    source
    1..67
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="129SV/Ev"
    /db_xref="taxon:10090"
    /clone="OS1240321"
    /cell_type="embryonic stem cell"
    /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match 51.0%; Score 14.8; DB 29; Length 67;
Best Local Similarity 44.4%; Pred. No. 2.8e+05;
Matches 12; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAGAUUCUUUUUGUAGCCCAAGGG 27
DB 2 AAGGATTTTITTTGGAGACNCGGG 28

RESULT 25
AL780467/c 70 bp mRNA linear EST 12-NOV-2003
LOCUS AL780467
DEFINITION AL780467 XGC-neurula Silurana tropicalis cDNA clone TNeu071b11 5',
mRNA sequence.
ACCESSION AL780467
VERSION AL780467.2 GI:38286361
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 70)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)

JOURNAL Unpublished (2003)
COMMENT On Jun 25, 2002 this sequence version replaced gi:21566171.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli DH10B
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TNeu071b11.picSP6
Sequencing primer: SP6.
FEATURES
    Location/Qualifiers
    1..70
    /organism="Silurana tropicalis"
    /mol_type="mRNA"
    /db_xref="taxon:8364"
    /clone="TNeu071b11"
    /dev_stage="neurula"
    /lab_host="Escherichia coli DH10B"
    /clone_lib="XGC-neurula"
    /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
    was oligo dt primed from Sug of poly A+ RNA from neurula.
    EcoRI-NotI cut cDNA was then ligated into pCS107 with
    EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
Query Match 51.0%; Score 14.8; DB 9; Length 70;
Best Local Similarity 46.2%; Pred. No. 2.8e+05;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGCGGU 29
DB 54 GACTTTGTTTGTGGCCCGCCGCGCT 29

RESULT 26
BZ289798/c 76 bp DNA linear GSS 24-OCT-2002
LOCUS BZ289798
DEFINITION SALK_023201.36.50.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_023201.36.50.x, genomic
survey sequence.
ACCESSION BZ289798
VERSION BZ289798.1 GI:24332044
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 76)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
    Location/Qualifiers
    1..76

```


KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS 1 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Siedler, H. and Weisshaar, B.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
AUTHORS A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
TITLE Unpublished
JOURNAL 3 (bases 1 to 53)
REFERENCE Strizhov, N., Rosso, M., Li, Y. and Weisshaar, B.
AUTHORS Direct Submission
TITLE Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
JOURNAL This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F7F22. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
COMMENT http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
1..53
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-252G08-014577"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
ORIGIN
Query Match 50.3%; Score 14.6; DB 29; Length 53;
Best Local Similarity 44.8%; Pred. No. 3.5e+05;
Matches 13; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Qy 1 AAAGAUCUUUUUUAAGCCCAAGGCU 29
Db 16 ATAATACCTATTCTAAGCCCTACCCCT 44

RESULT 30
BE970792 59 bp mRNA linear EST 04-OCT-2000
LOCUS 601680150R1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3950172 3',
DEFINITION mRNA sequence.
ACCESSION BE970792
VERSION BE970792.1 GI:10583725
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 59)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC816 row: d column: 13
High quality sequence stop: 57.

FEATURES source

1..59
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3950172"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 78"
/notes="Organ: pancreas; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccctcgcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptor sequences as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.2 Kb (range 0.5-4.0 Kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
Qy 6 UUCUUUUUUAAGCCCAAGG 26
Db 3 TTTTITTTTGAACCCCGAGG 23

ORIGIN

Query Match 50.3%; Score 14.6; DB 10; Length 59;
Best Local Similarity 47.6%; Pred. No. 3.4e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
Qy 6 UUCUUUUUUAAGCCCAAGG 26
Db 3 TTTTITTTTGAACCCCGAGG 23

RESULT 31

BE979345/c 61 bp mRNA linear EST 03-JUN-2002
LOCUS Ku33d12.y1 Strongyloides ratti PA female naive SL1 TOPO v1
DEFINITION Strongyloides ratti cDNA similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION

VERSION BE979345.1 GI:21315312

KEYWORDS

SOURCE Strongyloides ratti

ORGANISM

Strongyloides ratti

REFERENCE

AUTHORS 1 (bases 1 to 61)
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Stepien, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter

at Washington University, St. Louis. Parasitic adult females were collected from naive animals and provided by Dr. Mark Viney of University of Bristol, Bristol, UK (Mark.Viney@bristol.ac.uk).
Seq primer: SL1 primer.

FEATURES

Location/Qualifiers

```
1..61
/organism="Strongyloides ratti"
/mol_type="mRNA"
/db_xref="taxon:34506"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Strongyloides ratti PA female naive SL1 TOPO
v1"
/note="vector: pCR11-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCarter at Washington University,
St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR
products of size >400 nucleotides containing SL1 on the 5'
end and oligo(dT) on the 3' end were non-directionally
cloned into pCR11-TOPO(Invitrogen) following the TOPO TA
cloning protocol. Parasitic adult females were collected
from naive animals and provided by Dr. Mark Viney of
University of Bristol, Bristol, UK
(Mark.Viney@bristol.ac.uk)."
```

ORIGIN

```
Query Match      50.3%; Score 14.6; DB 13; Length 61;
Best Local Similarity 47.6%; Pred. No. 3.4e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY  2  AAGAUUCUUUUUUAAGCCCC 22
    |||:|:|:|:|:|:|:|:|:|
Db   32  AAAATGTTTTTGTAAAGCCC 12
```

```
RESULT 32
AL763793/c
LOCUS      AL763793
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-040F11-015225,
            genomic survey sequence.
VERSION    AL763793.1 GI:21514571
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  1  Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
            and Weissshaar,B.
            A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
            Unpublished
JOURNAL    2
REFERENCE  3  Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.
            A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
            Unpublished
JOURNAL    3  Strizhov,N., Rosso,M., Li,Y. and Weissshaar,B.
            Direct Submission
TITLE      Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
            Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
            This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone M4E13. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
            Location/Qualifiers
```

FEATURES

source

```
1..65
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-040F11-015225"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
```

ORIGIN

```
Query Match      50.3%; Score 14.6; DB 29; Length 65;
Best Local Similarity 48.3%; Pred. No. 3.4e+05;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY  1  AAGAUUCUUUUUUAAGCCCCCAAGGCU 29
    |||:|:|:|:|:|:|:|:|:|
Db   52  ATAAATCTTTAAGTAGCTCTAAAGGCT 24
```

RESULT 33

```
BZ768797/c
LOCUS      BZ768797
DEFINITION SALK_140745.49.75.n Arabidopsis thaliana T-DNA insertion lines
            Arabidopsis thaliana genomic clone SALK_140745.49.75.n, genomic
            survey sequence.
VERSION    BZ768797.1 GI:28942481
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  1  (bases 1 to 69)
            Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Leisse,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            T-DNA.
            Class: T-DNA tagged.
            Location/Qualifiers
```

FEATURES

source

```
1..69
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_140745.49.75.n"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more T-DNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tDNA\_protocols.html"
```

ORIGIN

```

Query Match          50.3%; Score 14.6; DB 28; Length 69;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUUGUAGCCC 21
    |||||:|:|:|:|:|:|
Db 48 AAAGATTCAATTTTAAAGCAC 28

RESULT 34
BZ768791/c
LOCUS          70 bp DNA linear GSS 13-MAR-2003
DEFINITION    SALK_140737.29.55.x.Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_140737.29.55.x, genomic
survey sequence.
ACCESSION     BZ768791
VERSION       BZ768791.1 GI:28942475
SOURCE        Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE     1 (bases 1 to 70)
AUTHORS       Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE         A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL       Unpublished (2001)
COMMENT       Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source           1..70
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_140737.29.55.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          50.3%; Score 14.6; DB 28; Length 70;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUUGUAGCCC 21
    |||||:|:|:|:|:|:|
Db 49 AAAGATTCAATTTTAAAGCAC 29

RESULT 35
BZ768795/c
LOCUS          70 bp DNA linear GSS 13-MAR-2003
DEFINITION    SALK_140742.35.20.x.Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_140742.35.20.x, genomic
survey sequence.
ACCESSION     BZ768795
VERSION       BZ768795.1 GI:28942475
SOURCE        Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE     1 (bases 1 to 70)
AUTHORS       Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE         A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL       Unpublished (2001)
COMMENT       Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source           1..70
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_140737.29.55.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          50.3%; Score 14.6; DB 28; Length 70;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUUGUAGCCC 21
    |||||:|:~:~:~:~:~:~
Db 49 AAAGATTCAATTTTAAAGCAC 29

RESULT 35
BZ768795/c
LOCUS          71 bp mRNA linear EST 10-FEB-2003
DEFINITION    IRJ35C09 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION     CB227161
VERSION       CB227161.1 GI:28297675
SOURCE        Bos taurus (cow)
ORGANISM      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE     1 (bases 1 to 71)
AUTHORS       Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Senses,C.W.,
Gordon,P.M.K. and Moore,S.S.
TITLE         Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
COMMENT       Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265

```

```

VERSION            BZ768795.1 GI:28942479
KEYWORDS           GSS.
SOURCE             Arabidopsis thaliana (thale cress)
ORGANISM           Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE          1 (bases 1 to 70)
AUTHORS           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE             A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL           Unpublished (2001)
COMMENT           Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES           Location/Qualifiers
     source         1..70
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_140742.35.20.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          50.3%; Score 14.6; DB 28; Length 70;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUUGUAGCCC 21
    |||||:|:~:~:~:~:~:~
Db 49 AAAGATTCAATTTTAAAGCAC 29

RESULT 36
CB227161/c
LOCUS          71 bp mRNA linear EST 10-FEB-2003
DEFINITION    IRJ35C09 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION     CB227161
VERSION       CB227161.1 GI:28297675
SOURCE        Bos taurus (cow)
ORGANISM      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE     1 (bases 1 to 71)
AUTHORS       Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Senses,C.W.,
Gordon,P.M.K. and Moore,S.S.
TITLE         Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
COMMENT       Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265

```

Email: stephen.moore@ualberta.ca
Insert Length: 71 Std Error: 0.00
POLYA=Yes

FEATURES

source

Location/Qualifiers

1. .71
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRF" strain"
/clone_lib="Bos taurus Rumex #1 library"
/note="Organ: Rumex; Vector: Uni-2ZAPXR; Site_1: EcoRI;
Site_2: Xho I"

ORIGIN

Query Match 50.3%; Score 14.6; DB 14; Length 71;
Best Local Similarity 47.6%; Pred. No. 3.3e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 6 UUUUUUUUUAAGCCCCAAGG 26

Db 55 TTTTGTGGAGTCCCAAGG 35

RESULT 37

AZ833202

LOCUS

2M0115E08F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC2M0115E08 F, genomic survey sequence.

ACCESSION

AZ833202

VERSION

AZ833202.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 71)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunnogenetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0115 row: E column: 08

Seq primer: CTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 71.

Location/Qualifiers

1. .71

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0115E08"

/sex="Male"

/lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.3%; Score 14.6; DB 28; Length 71;
Best Local Similarity 41.4%; Pred. No. 3.3e+05;
Matches 12; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AAAGAUUUUUUUAAGCCCCAAGGCU 29

Db 23 AAAGATTCCTTCTCCTAACTGCTAAATGTT 51

RESULT 38

AI696772

LOCUS

wc61d07.xl NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323117 3',
mRNA sequence.

ACCESSION

AI696772

VERSION

AI696772.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 75)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/dbp/image/image.html

Insert Length: 1931 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 51.

Location/Qualifiers

1. .75

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2323117"

/tissue_type="adenocarcinoma"

/lab_host="DH10B"

/clone_lib="NCI CGAP Pan1"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.72 Kb. Life technologies catalog #:

11548-013"

ORIGIN

Query Match 50.3%; Score 14.6; DB 9; Length 75;
Best Local Similarity 51.7%; Pred. No. 3.3e+05;
Matches 15; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AAAGAUUUUUUUAAGCCCCAAGGCU 29

```

Db      25 AATATAGTAGTGAATACCAACCAAGGCT 53
|||||: : : : ||| |||||:
RESULT 39
AL770832      80 bp      DNA      linear      GSS 19-JUN-2002
LOCUS      Arabidopsis thaliana T-DNA flanking sequence GK-175B08-013532,
DEFINITION genomic survey sequence.
ACCESSION AL770832
VERSION   AL770832.1
KEYWORDS  GSS.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
DEFINITION Arabidopsis thaliana; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 80)
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone F21P8. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             source
1..80
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-175B08-013532"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequences were
processed for submission. T-DNA derived sequences were
removed"
ORIGIN
Query Match      50.3%; Score 14.6; DB 29; Length 80;
Best Local Similarity 48.3%; Pred. No. 3.2e+05;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAAGAATUCUUUUAAGCCCAAGGCGU 29
|||||: : : : ||| |||||:
Db 39 AAACAGTCTTTTCACACCTATGGGAT 67
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RESULT 40
BX662819      80 bp      DNA      linear      GSS 09-OCT-2003
LOCUS      Arabidopsis thaliana T-DNA flanking sequence GK-708H02-022874,
DEFINITION genomic survey sequence.
ACCESSION BX662819
VERSION   BX662819.1
KEYWORDS  GSS.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
DEFINITION Arabidopsis thaliana; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 80)
Direct Submission
Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone MM17. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             source
1..80
/mol_type="genomic DNA"
/strain="Columbia 0"
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/clone="GK-708H02-022874"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequences were
processed for submission. T-DNA derived sequences were
removed"
ORIGIN
Query Match      50.3%; Score 14.6; DB 29; Length 80;
Best Local Similarity 47.6%; Pred. No. 3.2e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 9 UUUUUGUAGCCCAAGGCGU 29
|||||: : : : ||| |||||:
Db 27 TTTTGTATATCTCAAGGCGT 47
|||||: : : : ||| |||||:

Search completed: April 18, 2004, 09:59:30
Job time : 1553.67 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 08:41:44 ; Search time 159.667 Seconds
(without alignments)

812.711 Million cell updates/sec

Title: US-09-310-844C-25

Perfect score: 29

Sequence: 1 aaagaucuuuuuuaagcccaaggcu 29

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 1657369

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	15.2	52.4	47	15	US-10-349-143-1097
C 5	15.2	52.4	60	10	US-09-908-975-18725
C 6	15	51.7	39	14	US-10-116-519-18
C 7	15	51.7	60	10	US-09-908-975-12187
C 8	15	51.7	65	10	US-09-908-975-4580
C 9	14.8	51.0	29	10	US-09-839-478-31
C 10	14.6	50.3	25	14	US-10-005-530-18
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C 12	14.6	50.3	60	10	US-09-908-975-18114
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C 14	14.6	50.3	60	16	US-10-231-494-24
C 15	14.6	50.3	75	9	US-09-864-761-23841

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31	10	US-09-740-332-5660	49.7	14.4	C 17
31	10	US-09-817-879-5660	49.7	14.4	C 18
65	10	US-09-908-975-3924	49.7	14.4	C 19
65	10	US-09-908-975-30555	49.7	14.4	C 20
25	9	US-09-827-998-1098	49.0	14.2	C 21
25	9	US-09-827-998-1099	49.0	14.2	C 22
25	9	US-09-827-998-1100	49.0	14.2	C 23
25	9	US-09-827-998-1101	49.0	14.2	C 24
25	9	US-09-827-998-1102	49.0	14.2	C 25
25	9	US-09-827-998-1103	49.0	14.2	C 26
25	9	US-09-827-998-1104	49.0	14.2	C 27
25	12	US-10-575-685-1098	49.0	14.2	C 28
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65	14	US-10-032-585-500	49.0	14.2	C 47
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38	14	US-10-122-706-20	46.9	13.6	C 79
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273	12.6	43.4	36	12	US-10-369-100-44	Sequence 44, Appl	c 346	12.4	42.8	48	15	US-10-456-129-37	Sequence 37, Appl
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295	12.6	43.4	56	15	US-10-131-827-6946	Sequence 6846, Ap	c 368	12.2	42.1	17	12	US-10-675-685-282	Sequence 282, App
296	12.6	43.4	56	15	US-10-131-827-7142	Sequence 7142, Ap	c 369	12.2	42.1	17	12	US-10-675-685-283	Sequence 283, App
297	12.6	43.4	56	15	US-10-131-827-7436	Sequence 7436, Ap	c 370	12.2	42.1	17	12	US-09-927-046-677	Sequence 677, App
298	12.6	43.4	56	15	US-10-131-827-7515	Sequence 7515, Ap	c 371	12.2	42.1	17	12	US-09-263-959-1168	Sequence 1168, Ap
299	12.6	43.4	60	10	US-09-908-975-8677	Sequence 8677, Ap	c 372	12.2	42.1	20	9	US-09-263-959-1168	Sequence 1168, Ap
300	12.6	43.4	60	10	US-09-908-975-11206	Sequence 11206, A	c 373	12.2	42.1	20	15	US-10-289-762-6382	Sequence 6382, Ap
301	12.6	43.4	60	10	US-09-908-975-11727	Sequence 11727, A	c 374	12.2	42.1	22	12	US-10-092-900A-691	Sequence 691, App
302	12.6	43.4	60	10	US-09-908-975-12876	Sequence 12876, A	c 375	12.2	42.1	25	9	US-09-827-998-1096	Sequence 1096, Ap
303	12.6	43.4	60	10	US-09-908-975-19799	Sequence 19799, A	c 376	12.2	42.1	25	9	US-09-827-998-1106	Sequence 1106, Ap
304	12.6	43.4	60	10	US-09-908-975-20618	Sequence 20618, A	c 377	12.2	42.1	25	10	US-09-730-2898-1697	Sequence 1697, Ap
305	12.6	43.4	63	14	US-09-908-975-31392	Sequence 31392, A	c 378	12.2	42.1	25	10	US-09-730-2898-3611	Sequence 3611, Ap
306	12.6	43.4	63	14	US-10-078-090-42	Sequence 42, Appl	c 379	12.2	42.1	25	12	US-10-675-685-1096	Sequence 1096, Ap
307	12.6	43.4	65	10	US-09-908-975-156	Sequence 156, App	c 380	12.2	42.1	25	12	US-10-675-685-1106	Sequence 1106, Ap

381	12.2	42.1	25	14	US-10-098-263B-17955	Sequence 17955, A	C 454	12.2	42.1	60	10	US-09-908-975-8204	Sequence 8204, Ap
382	12.2	42.1	25	14	US-10-098-263B-18902	Sequence 18902, A	C 455	12.2	42.1	60	10	US-09-908-975-13235	Sequence 13235, A
C 383	12.2	42.1	25	14	US-10-098-263B-61220	Sequence 61220, A	C 456	12.2	42.1	60	10	US-09-908-975-14519	Sequence 14519, A
384	12.2	42.1	25	14	US-10-098-263B-65119	Sequence 65119, A	C 457	12.2	42.1	60	10	US-09-908-975-15116	Sequence 15116, A
C 385	12.2	42.1	25	14	US-10-098-263B-83813	Sequence 83813, A	C 458	12.2	42.1	60	10	US-09-908-975-15205	Sequence 15205, A
C 386	12.2	42.1	25	14	US-10-440-066-4	Sequence 4, Appli	C 459	12.2	42.1	60	10	US-09-908-975-15205	Sequence 15205, A
387	12.2	42.1	28	9	US-09-984-863-4	Sequence 4, Appli	C 460	12.2	42.1	60	10	US-09-908-975-15340	Sequence 15340, A
C 388	12.2	42.1	29	9	US-09-875-461-30	Sequence 30, Appli	C 461	12.2	42.1	60	10	US-09-908-975-15340	Sequence 15340, A
C 389	12.2	42.1	29	9	US-10-336-638-323	Sequence 323, Appl	C 462	12.2	42.1	60	10	US-09-908-975-15340	Sequence 15340, A
C 390	12.2	42.1	30	9	US-09-465-802-6	Sequence 6, Appli	C 463	12.2	42.1	60	10	US-09-908-975-15340	Sequence 15340, A
C 391	12.2	42.1	30	9	US-09-898-627-2	Sequence 2, Appli	C 464	12.2	42.1	60	10	US-09-908-975-15340	Sequence 15340, A
C 392	12.2	42.1	30	9	US-09-948-491A-4	Sequence 4, Appli	C 465	12.2	42.1	60	10	US-09-908-975-15340	Sequence 15340, A
C 393	12.2	42.1	31	9	US-09-801-274-808	Sequence 808, Appl	C 466	12.2	42.1	62	14	US-10-330-772-22	Sequence 22, Appli
C 394	12.2	42.1	31	9	US-09-780-164-2136	Sequence 2136, Ap	C 467	12.2	42.1	62	14	US-10-330-772-22	Sequence 22, Appli
C 395	12.2	42.1	31	10	US-09-740-332-8853	Sequence 8853, Ap	C 468	12.2	42.1	63	15	US-10-027-632-176912	Sequence 176912, A
C 396	12.2	42.1	31	10	US-09-740-332-9111	Sequence 9111, Ap	C 469	12.2	42.1	63	15	US-10-027-632-176912	Sequence 176912, A
C 397	12.2	42.1	31	10	US-09-740-332-9223	Sequence 9223, Ap	C 470	12.2	42.1	65	10	US-09-908-975-25878	Sequence 25878, A
C 398	12.2	42.1	31	10	US-09-817-879-8853	Sequence 8853, Ap	C 471	12.2	42.1	65	10	US-09-908-975-25878	Sequence 25878, A
C 399	12.2	42.1	31	10	US-09-817-879-9111	Sequence 9111, Ap	C 472	12.2	42.1	65	10	US-09-908-975-25878	Sequence 25878, A
C 400	12.2	42.1	31	10	US-09-817-879-9223	Sequence 9223, Ap	C 473	12.2	42.1	65	10	US-09-908-975-25878	Sequence 25878, A
C 401	12.2	42.1	31	14	US-10-163-552-1089	Sequence 1089, Ap	C 474	12.2	42.1	65	10	US-09-908-975-25878	Sequence 25878, A
C 402	12.2	42.1	31	14	US-10-163-552-1254	Sequence 1254, Ap	C 475	12.2	42.1	65	14	US-10-032-585-1179	Sequence 1179, Ap
C 403	12.2	42.1	31	14	US-10-163-552-1254	Sequence 1254, Ap	C 476	12.2	42.1	65	14	US-10-032-585-1179	Sequence 1179, Ap
C 404	12.2	42.1	31	14	US-10-238-700-3845	Sequence 3845, Ap	C 477	12.2	42.1	65	14	US-10-032-585-1179	Sequence 1179, Ap
C 405	12.2	42.1	32	9	US-09-842-552-36	Sequence 36, Appli	C 478	12.2	42.1	65	14	US-10-032-585-1179	Sequence 1179, Ap
C 406	12.2	42.1	32	9	US-09-798-042-77	Sequence 77, Appli	C 479	12.2	42.1	66	12	US-09-837-306-412	Sequence 306, Ap
C 407	12.2	42.1	32	12	US-09-953-108-77	Sequence 77, Appli	C 480	12.2	42.1	66	12	US-09-837-306-412	Sequence 306, Ap
C 408	12.2	42.1	32	14	US-10-384-948-8	Sequence 8, Appli	C 481	12.2	42.1	66	15	US-10-106-698-3846	Sequence 3846, Ap
C 409	12.2	42.1	34	9	US-09-948-491A-2	Sequence 2, Appli	C 482	12.2	42.1	66	15	US-10-106-698-3846	Sequence 3846, Ap
C 410	12.2	42.1	34	12	US-10-037-632-176735	Sequence 176735, A	C 483	12.2	42.1	72	10	US-09-747-377-160	Sequence 160, Ap
C 411	12.2	42.1	34	14	US-10-234-007-18	Sequence 18, Appli	C 484	12.2	42.1	72	14	US-10-105-613-160	Sequence 160, Ap
C 412	12.2	42.1	34	15	US-10-027-632-176735	Sequence 176735, A	C 485	12.2	42.1	73	14	US-10-142-283-91	Sequence 91, Appli
C 413	12.2	42.1	35	12	US-10-027-632-176735	Sequence 176735, A	C 486	12.2	42.1	73	14	US-10-142-283-91	Sequence 91, Appli
C 414	12.2	42.1	35	15	US-10-027-632-176735	Sequence 176735, A	C 487	12.2	42.1	74	9	US-09-783-590-11398	Sequence 11398, A
C 415	12.2	42.1	37	14	US-10-156-306-2647	Sequence 2647, Ap	C 488	12.2	42.1	75	9	US-09-783-590-11398	Sequence 11398, A
C 416	12.2	42.1	37	14	US-10-156-306-2647	Sequence 2647, Ap	C 489	12.2	42.1	80	10	US-09-047-966-61	Sequence 61, Appli
C 417	12.2	42.1	38	10	US-09-877-478-4331	Sequence 4331, Ap	C 490	12.2	42.1	80	10	US-09-047-966-61	Sequence 61, Appli
C 418	12.2	42.1	41	14	US-10-342-902-4331	Sequence 4331, Ap	C 491	12.2	42.1	80	10	US-09-047-966-61	Sequence 61, Appli
C 419	12.2	42.1	41	15	US-10-005-956-933	Sequence 933, Appli	C 492	12.2	42.1	18	14	US-10-056-908-26	Sequence 26, Appli
C 420	12.2	42.1	41	15	US-10-310-740-8	Sequence 8, Appli	C 493	12.2	42.1	20	16	US-09-824-322B-198	Sequence 198, Appl
C 421	12.2	42.1	42	15	US-10-310-740-8	Sequence 8, Appli	C 494	12.2	42.1	20	16	US-10-210-290-14	Sequence 14, Appli
C 422	12.2	42.1	43	14	US-10-142-283-88	Sequence 88, Appli	C 495	12.2	42.1	21	14	US-10-092-900A-517	Sequence 517, Appl
C 423	12.2	42.1	43	14	US-10-032-585-694	Sequence 694, Appl	C 496	12.2	42.1	21	14	US-10-015-979-16	Sequence 16, Appli
C 424	12.2	42.1	44	12	US-09-047-966-58	Sequence 58, Appli	C 497	12.2	42.1	21	15	US-10-349-143-6777	Sequence 6777, Ap
C 425	12.2	42.1	47	12	US-10-294-934-500	Sequence 500, Appl	C 498	12.2	42.1	21	15	US-10-349-143-6777	Sequence 6777, Ap
C 426	12.2	42.1	47	12	US-10-294-934-592	Sequence 592, Appl	C 499	12.2	42.1	23	14	US-10-214-417A-21	Sequence 21, Appli
C 427	12.2	42.1	47	15	US-10-170-097-1000	Sequence 1000, Ap	C 500	12.2	42.1	23	14	US-10-214-417A-21	Sequence 21, Appli
C 428	12.2	42.1	47	15	US-10-349-143-2286	Sequence 2286, Ap	C 501	12.2	42.1	25	14	US-10-098-263B-15368	Sequence 15368, A
C 429	12.2	42.1	48	15	US-10-338-366-27	Sequence 258, Ap	C 502	12.2	42.1	25	14	US-10-098-263B-15368	Sequence 15368, A
C 430	12.2	42.1	50	15	US-10-131-827-48	Sequence 48, Appli	C 503	12.2	42.1	25	14	US-10-098-263B-20227	Sequence 20227, A
C 431	12.2	42.1	50	15	US-10-131-827-399	Sequence 399, Appl	C 504	12.2	42.1	25	14	US-10-098-263B-20227	Sequence 20227, A
C 432	12.2	42.1	50	15	US-10-131-827-1361	Sequence 1361, Ap	C 505	12.2	42.1	25	14	US-10-098-263B-30307	Sequence 30307, A
C 433	12.2	42.1	50	15	US-10-131-827-1636	Sequence 1636, Ap	C 506	12.2	42.1	25	14	US-10-098-263B-30307	Sequence 30307, A
C 434	12.2	42.1	50	15	US-10-131-827-1779	Sequence 1779, Ap	C 507	12.2	42.1	25	14	US-10-098-263B-45081	Sequence 45081, A
C 435	12.2	42.1	50	15	US-10-131-827-3573	Sequence 3573, Ap	C 508	12.2	42.1	25	14	US-10-098-263B-45081	Sequence 45081, A
C 436	12.2	42.1	50	15	US-10-131-827-3573	Sequence 3573, Ap	C 509	12.2	42.1	25	14	US-10-098-263B-47161	Sequence 47161, A
C 437	12.2	42.1	50	15	US-10-131-827-4124	Sequence 4124, Ap	C 510	12.2	42.1	25	14	US-10-098-263B-80471	Sequence 80471, A
C 438	12.2	42.1	50	15	US-10-131-827-4503	Sequence 4503, Ap	C 511	12.2	42.1	25	14	US-10-098-263B-80471	Sequence 80471, A
C 439	12.2	42.1	50	15	US-10-131-827-7998	Sequence 7998, Ap	C 512	12.2	42.1	25	14	US-10-098-263B-110175	Sequence 110175, A
C 440	12.2	42.1	51	12	US-09-951-061A-16	Sequence 16, Appli	C 513	12.2	42.1	25	14	US-10-098-263B-110175	Sequence 110175, A
C 441	12.2	42.1	51	12	US-10-441-788-16	Sequence 16, Appli	C 514	12.2	42.1	25	12	US-10-384-431-51	Sequence 51, Appli
C 442	12.2	42.1	51	14	US-10-267-384-16	Sequence 16, Appli	C 515	12.2	42.1	31	9	US-09-745-008-7	Sequence 7, Appli
C 443	12.2	42.1	51	14	US-10-235-175-23	Sequence 23, Appli	C 516	12.2	42.1	31	9	US-09-745-008-7	Sequence 7, Appli
C 444	12.2	42.1	55	14	US-10-199-820-197	Sequence 197, Appl	C 517	12.2	42.1	31	9	US-09-745-008-7	Sequence 7, Appli
C 445	12.2	42.1	57	14	US-10-281-479A-96	Sequence 96, Appli	C 518	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 446	12.2	42.1	57	14	US-10-275-180A-96	Sequence 96, Appli	C 519	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 447	12.2	42.1	57	14	US-10-286-132A-96	Sequence 96, Appli	C 520	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 448	12.2	42.1	59	10	US-09-991-936-1182	Sequence 1182, Ap	C 521	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 449	12.2	42.1	59	9	US-09-912-678-35	Sequence 35, Appli	C 522	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 450	12.2	42.1	59	9	US-09-466-035-35	Sequence 35, Appli	C 523	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 451	12.2	42.1	60	10	US-09-908-975-4956	Sequence 4956, Ap	C 524	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 452	12.2	42.1	60	10	US-09-908-975-6077	Sequence 6077, Ap	C 525	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap
C 453	12.2	42.1	60	10	US-09-908-975-7149	Sequence 7149, Ap	C 526	12.2	42.1	31	10	US-09-864-785-2198	Sequence 2198, Ap

C 527	12	41.4	31	10	US-09-745-237A-3311	Sequence 3311, Ap	C 600	12	41.4	65	14	US-10-032-585-3007	Sequence 3007, Ap
C 528	12	41.4	31	10	US-09-745-237A-3545	Sequence 3545, Ap	C 601	12	41.4	65	14	US-10-032-585-3405	Sequence 3405, Ap
C 529	12	41.4	31	10	US-09-817-879-5178	Sequence 5178, Ap	C 602	12	41.4	65	14	US-10-032-585-3479	Sequence 3479, Ap
C 530	12	41.4	31	10	US-09-817-879-5224	Sequence 5224, Ap	C 603	12	41.4	66	9	US-09-858-994-10	Sequence 10, Appl
C 531	12	41.4	31	10	US-09-817-879-5478	Sequence 5478, Ap	C 604	12	41.4	66	9	US-09-858-994-11	Sequence 11, Appl
C 532	12	41.4	31	10	US-09-817-879-5632	Sequence 5632, Ap	C 605	12	41.4	74	10	US-09-911-132A-32	Sequence 32, Appl
C 533	12	41.4	31	10	US-09-817-879-6410	Sequence 6410, Ap	C 606	12	41.4	75	9	US-09-864-761-28472	Sequence 28472, A
C 534	12	41.4	31	10	US-09-817-879-6583	Sequence 6583, Ap	C 607	12	41.4	75	9	US-09-864-761-28699	Sequence 28699, A
C 535	12	41.4	31	10	US-09-817-879-8938	Sequence 8938, Ap	C 608	12	41.4	78	9	US-09-858-994-4	Sequence 4, Appl
C 536	12	41.4	31	12	US-10-342-903-4558	Sequence 4558, Ap	C 609	12	41.4	78	9	US-09-858-994-5	Sequence 5, Appl
C 537	12	41.4	33	9	US-09-875-494-22	Sequence 22, Appl	C 610	12	41.4	78	9	US-09-922-217-324	Sequence 324, App
C 538	12	41.4	34	14	US-10-058-825A-1	Sequence 1, Appl	C 611	12	41.4	78	9	US-09-833-363-324	Sequence 324, App
C 539	12	41.4	37	9	US-09-677-478-3639	Sequence 4, Appl	C 612	12	41.4	78	13	US-10-025-380-324	Sequence 324, App
C 540	12	41.4	38	10	US-09-677-478-3639	Sequence 3639, Ap	C 613	12	41.4	78	15	US-10-448-250-67	Sequence 67, Appl
C 541	12	41.4	38	14	US-10-342-903-2339	Sequence 2339, Ap	C 614	12	41.4	79	15	US-10-406-903-125	Sequence 125, App
C 542	12	41.4	38	14	US-10-156-308-2339	Sequence 2339, Ap	C 615	12	41.4	80	9	US-09-864-761-24511	Sequence 24511, A
C 543	12	41.4	38	14	US-10-230-008-890	Sequence 890, App	C 616	11.8	40.7	17	9	US-09-827-998-284	Sequence 284, App
C 544	12	41.4	40	15	US-10-411-066-51	Sequence 51, Appl	C 617	11.8	40.7	17	9	US-09-827-998-285	Sequence 285, App
C 545	12	41.4	41	15	US-10-453-827-99	Sequence 99, Appl	C 618	11.8	40.7	17	12	US-10-675-685-284	Sequence 284, App
C 546	12	41.4	41	14	US-10-005-955-275	Sequence 275, App	C 619	11.8	40.7	17	12	US-10-675-685-285	Sequence 285, App
C 547	12	41.4	45	14	US-10-123-706-10	Sequence 10, Appl	C 620	11.8	40.7	20	10	US-09-954-679-80	Sequence 80, Appl
C 548	12	41.4	47	8	US-08-935-377-35	Sequence 35, Appl	C 621	11.8	40.7	20	12	US-09-960-143-68	Sequence 68, Appl
C 549	12	41.4	47	8	US-08-469-583A-3	Sequence 3, Appl	C 622	11.8	40.7	20	14	US-10-251-598-91	Sequence 0, Appl
C 550	12	41.4	47	9	US-09-822-250-35	Sequence 35, Appl	C 623	11.8	40.7	21	9	US-09-785-081-363	Sequence 363, App
C 551	12	41.4	47	10	US-09-818-991-32	Sequence 32, Appl	C 624	11.8	40.7	21	9	US-09-952-571-1	Sequence 1, Appl
C 552	12	41.4	47	12	US-10-294-934-703	Sequence 703, App	C 625	11.8	40.7	21	15	US-10-435-696-279	Sequence 279, App
C 553	12	41.4	47	14	US-10-277-161-32	Sequence 32, Appl	C 626	11.8	40.7	24	10	US-09-940-185-2136	Sequence 2136, Ap
C 554	12	41.4	47	15	US-10-349-143-3352	Sequence 3352, Ap	C 627	11.8	40.7	25	9	US-09-827-998-1107	Sequence 1107, Ap
C 555	12	41.4	50	14	US-10-068-666A-23	Sequence 23, Appl	C 628	11.8	40.7	25	9	US-09-827-998-1108	Sequence 1108, Ap
C 556	12	41.4	50	15	US-10-131-827-1131	Sequence 1131, Ap	C 629	11.8	40.7	25	10	US-09-730-2898-1598	Sequence 1598, Ap
C 557	12	41.4	50	15	US-10-131-827-1397	Sequence 1397, Ap	C 630	11.8	40.7	25	10	US-09-730-2898-1599	Sequence 1599, Ap
C 558	12	41.4	50	15	US-10-131-827-2374	Sequence 2374, Ap	C 631	11.8	40.7	25	10	US-09-730-2898-3612	Sequence 3612, Ap
C 559	12	41.4	50	15	US-10-131-827-2937	Sequence 2937, Ap	C 632	11.8	40.7	25	10	US-09-730-2898-3613	Sequence 3613, Ap
C 560	12	41.4	50	15	US-10-131-827-4047	Sequence 4047, Ap	C 633	11.8	40.7	25	10	US-09-940-185-4466	Sequence 4466, Ap
C 561	12	41.4	51	9	US-09-945-952A-33	Sequence 33, Appl	C 634	11.8	40.7	25	12	US-10-675-685-1107	Sequence 1107, Ap
C 562	12	41.4	51	9	US-09-945-952A-35	Sequence 35, Appl	C 635	11.8	40.7	25	12	US-10-675-685-1108	Sequence 1108, Ap
C 563	12	41.4	51	14	US-10-233-942-33	Sequence 33, Appl	C 636	11.8	40.7	25	14	US-10-098-2638-15933	Sequence 15933, A
C 564	12	41.4	51	14	US-10-233-942-35	Sequence 35, Appl	C 637	11.8	40.7	25	14	US-10-098-2638-15939	Sequence 15939, A
C 565	12	41.4	55	8	US-08-781-986A-1690	Sequence 1690, Ap	C 638	11.8	40.7	25	14	US-10-098-2638-27791	Sequence 27791, A
C 566	12	41.4	55	8	US-08-781-986A-5024	Sequence 5024, Ap	C 639	11.8	40.7	25	14	US-10-098-2638-41638	Sequence 41638, A
C 567	12	41.4	55	12	US-10-329-624-1690	Sequence 1690, Ap	C 640	11.8	40.7	25	14	US-10-098-2638-49954	Sequence 49954, A
C 568	12	41.4	55	12	US-10-329-624-5024	Sequence 5024, Ap	C 641	11.8	40.7	25	14	US-10-098-2638-51513	Sequence 51513, A
C 569	12	41.4	56	14	US-10-106-698-4210	Sequence 4210, Ap	C 642	11.8	40.7	25	14	US-10-098-2638-65910	Sequence 65910, A
C 570	12	41.4	58	10	US-09-907-111-263	Sequence 263, App	C 643	11.8	40.7	25	14	US-10-098-2638-77900	Sequence 77900, A
C 571	12	41.4	58	8	US-08-459-455-31	Sequence 31, Appl	C 644	11.8	40.7	25	14	US-10-098-2638-96774	Sequence 96774, A
C 572	12	41.4	60	10	US-09-908-975-4939	Sequence 4939, Ap	C 645	11.8	40.7	25	14	US-10-032-585-4401	Sequence 4401, Ap
C 573	12	41.4	60	10	US-09-908-975-6817	Sequence 6817, Ap	C 646	11.8	40.7	26	10	US-09-935-464-73	Sequence 73, Appl
C 574	12	41.4	60	10	US-09-908-975-7835	Sequence 7835, Ap	C 647	11.8	40.7	26	12	US-10-447-476-9	Sequence 9, Appl
C 575	12	41.4	60	10	US-09-908-975-8725	Sequence 8725, Ap	C 648	11.8	40.7	26	14	US-10-164-776-14	Sequence 14, Appl
C 576	12	41.4	60	10	US-09-908-975-15308	Sequence 15308, A	C 649	11.8	40.7	27	14	US-10-205-713A-3	Sequence 3, Appl
C 577	12	41.4	60	10	US-09-908-975-15308	Sequence 15308, A	C 650	11.8	40.7	28	9	US-09-949-145-73	Sequence 73, Appl
C 578	12	41.4	60	10	US-09-908-975-17068	Sequence 17068, A	C 651	11.8	40.7	28	13	US-10-020-540A-10	Sequence 10, Appl
C 579	12	41.4	60	10	US-09-908-975-17499	Sequence 17499, A	C 652	11.8	40.7	30	9	US-09-770-517C-22	Sequence 22, Appl
C 580	12	41.4	60	10	US-09-908-975-17575	Sequence 17575, A	C 653	11.8	40.7	31	9	US-09-801-274-1112	Sequence 1112, Ap
C 581	12	41.4	60	10	US-09-908-975-20830	Sequence 20830, A	C 654	11.8	40.7	31	9	US-09-928-457-48	Sequence 48, Appl
C 582	12	41.4	60	10	US-09-908-975-20875	Sequence 20875, A	C 655	11.8	40.7	31	9	US-09-864-785-2464	Sequence 2464, Ap
C 583	12	41.4	60	10	US-09-908-975-21435	Sequence 21435, A	C 656	11.8	40.7	31	10	US-09-730-2898-3190	Sequence 3190, Ap
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C 585	12	41.4	60	12	US-10-660-860-11	Sequence 11, Appl	C 658	11.8	40.7	31	10	US-09-730-2898-3207	Sequence 3207, Ap
C 586	12	41.4	61	14	US-09-971-101A-14	Sequence 14, Appl	C 659	11.8	40.7	31	10	US-09-730-2898-3207	Sequence 3207, Ap
C 587	12	41.4	61	14	US-10-349-508-66	Sequence 66, Appl	C 660	11.8	40.7	31	10	US-09-780-533A-5735	Sequence 5735, Ap
C 588	12	41.4	61	15	US-10-437-169-66	Sequence 66, Appl	C 661	11.8	40.7	31	10	US-09-848-754A-6855	Sequence 6855, Ap
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C 590	12	41.4	65	10	US-09-908-975-1535	Sequence 1535, Ap	C 663	11.8	40.7	31	10	US-09-848-754A-6861	Sequence 6861, Ap
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C 592	12	41.4	65	10	US-09-908-975-23816	Sequence 23816, A	C 665	11.8	40.7	31	10	US-09-740-332-4879	Sequence 4879, Ap
C 593	12	41.4	65	10	US-09-908-975-25747	Sequence 25747, A	C 666	11.8	40.7	31	10	US-09-740-332-4879	Sequence 4879, Ap
C 594	12	41.4	65	10	US-09-908-975-26521	Sequence 26521, A	C 667	11.8	40.7	31	10	US-09-740-332-6169	Sequence 6169, Ap
C 595	12	41.4	65	10	US-09-908-975-27006	Sequence 27006, A	C 668	11.8	40.7	31	10	US-09-740-332-6171	Sequence 6171, Ap
C 596	12	41.4	65	10	US-09-908-975-29018	Sequence 29018, A	C 669	11.8	40.7	31	10	US-09-740-332-7368	Sequence 7368, Ap
C 597	12	41.4	65	10	US-09-908-975-29078	Sequence 29078, A	C 670	11.8	40.7	31	10	US-09-740-332-7377	Sequence 7377, Ap
C 598	12	41.4	65	10	US-09-908-975-29424	Sequence 29424, A	C 671	11.8	40.7	31	10	US-09-792-818-1619	Sequence 1619, Ap
C 599	12	41.4	65	14	US-10-032-585-543	Sequence 543, App	C 672	11.8	40.7	31	10	US-09-817-879-4879	Sequence 4879, Ap

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C 674	11.8	40.7	31	10	US-09-817-879-6171	Sequence 6171, Ap	C 747	11.8	40.7	53	14	US-10-300-899-52	Sequence 52, Appl
C 675	11.8	40.7	31	10	US-09-817-879-7114	Sequence 7114, Ap	C 748	11.8	40.7	54	11	US-09-405-032-105	Sequence 105, Appl
C 676	11.8	40.7	31	10	US-09-817-879-7368	Sequence 7368, Ap	C 749	11.8	40.7	57	14	US-10-222-026A-7	Sequence 7, Appl
C 677	11.8	40.7	31	10	US-09-817-879-7377	Sequence 7377, Ap	C 750	11.8	40.7	59	14	US-10-072-622-15	Sequence 15, Appl
C 678	11.8	40.7	31	14	US-10-005-530-20	Sequence 20, Appl	C 751	11.8	40.7	60	10	US-09-908-975-6479	Sequence 6479, Ap
C 679	11.8	40.7	31	14	US-10-463-552-1485	Sequence 1485, Ap	C 752	11.8	40.7	60	10	US-09-908-975-7234	Sequence 7234, Ap
C 680	11.8	40.7	31	14	US-10-238-700-2351	Sequence 2351, Ap	C 753	11.8	40.7	60	10	US-09-908-975-8792	Sequence 8792, Ap
C 681	11.8	40.7	31	14	US-10-238-700-3723	Sequence 3723, Ap	C 754	11.8	40.7	60	10	US-09-908-975-9821	Sequence 9821, Ap
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C 683	11.8	40.7	32	14	US-10-389-135A-113	Sequence 113, Appl	C 756	11.8	40.7	60	10	US-09-908-975-10190	Sequence 10628, A
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C 693	11.8	40.7	38	10	US-09-877-478-3793	Sequence 3793, Ap	C 766	11.8	40.7	60	10	US-09-908-975-31429	Sequence 36, Appl
C 694	11.8	40.7	38	10	US-09-930-423-2694	Sequence 2694, Ap	C 767	11.8	40.7	60	12	US-10-332-340-36	Sequence 32, Appl
C 695	11.8	40.7	38	10	US-09-930-423-3039	Sequence 3039, Ap	C 768	11.8	40.7	60	14	US-10-187-394-32	Sequence 362, Appl
C 696	11.8	40.7	38	10	US-09-780-164-1388	Sequence 1388, Ap	C 769	11.8	40.7	61	10	US-09-849-928-362	Sequence 362, Appl
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C 699	11.8	40.7	38	12	US-10-342-902-2945	Sequence 2945, Ap	C 772	11.8	40.7	62	12	US-10-075-028B-15	Sequence 13, Appl
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C 701	11.8	40.7	38	14	US-10-102-720-10	Sequence 10, Appl	C 774	11.8	40.7	62	13	US-10-027-632-58365	Sequence 58365, A
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C 709	11.8	40.7	43	14	US-10-032-585-795	Sequence 795, Appl	C 782	11.8	40.7	65	10	US-09-908-975-3543	Sequence 3615, Ap
C 710	11.8	40.7	43	14	US-10-032-585-1806	Sequence 1806, Ap	C 783	11.8	40.7	65	10	US-09-908-975-3615	Sequence 3856, Ap
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C 713	11.8	40.7	43	15	US-10-361-208-57	Sequence 57, Appl	C 786	11.8	40.7	65	10	US-09-908-975-4099	Sequence 48223, A
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C 719	11.8	40.7	46	15	US-10-027-632-177846	Sequence 177846, Ap	C 792	11.8	40.7	65	10	US-09-908-975-30112	Sequence 30112, A
C 720	11.8	40.7	47	9	US-09-756-095-71	Sequence 71, Appl	C 793	11.8	40.7	65	10	US-09-908-975-30112	Sequence 31139, A
C 721	11.8	40.7	47	10	US-09-941-432-71	Sequence 71, Appl	C 794	11.8	40.7	65	10	US-09-908-975-31139	Sequence 31230, A
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C 723	11.8	40.7	47	10	US-09-941-432-114	Sequence 114, Appl	C 796	11.8	40.7	65	14	US-10-032-585-176	Sequence 176, Appl
C 724	11.8	40.7	47	10	US-09-941-432-115	Sequence 115, Appl	C 797	11.8	40.7	65	14	US-10-032-585-1191	Sequence 1191, Appl
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C 728	11.8	40.7	47	10	US-09-838-858-71	Sequence 71, Appl	C 801	11.8	40.7	65	14	US-10-032-585-2537	Sequence 2537, Ap
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C 732	11.8	40.7	47	15	US-10-349-143-734	Sequence 734, Appl	C 805	11.8	40.7	65	14	US-09-295-176-5	Sequence 5, Appl
C 733	11.8	40.7	47	15	US-10-349-143-2486	Sequence 2486, Ap	C 806	11.8	40.7	66	13	US-10-017-145-10	Sequence 10, Appl
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C 735	11.8	40.7	48	9	US-09-892-1888-12	Sequence 12, Appl	C 808	11.8	40.7	66	14	US-10-300-683-520	Sequence 120, Appl
C 736	11.8	40.7	48	12	US-10-374-784A-10	Sequence 10, Appl	C 809	11.8	40.7	72	12	US-10-670-503-12	Sequence 52, Appl
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C 739	11.8	40.7	50	15	US-10-131-827-1428	Sequence 1428, Ap	C 812	11.8	40.7	77	14	US-10-029-386-18275	Sequence 9, Appl
C 740	11.8	40.7	50	15	US-10-131-827-1561	Sequence 1561, Ap	C 813	11.8	40.7	79	9	US-09-887-3848-9	Sequence 9, Appl
C 741	11.8	40.7	50	15	US-10-131-827-2462	Sequence 2462, Ap	C 814	11.8	40.7	80	14	US-10-029-386-18275	Sequence 8, Appl
C 742	11.8	40.7	50	15	US-10-131-827-2721	Sequence 2721, Ap	C 815	11.6	40.0	80	14	US-09-945-952A-8	Sequence 39, Appl
C 743	11.8	40.7	50	15	US-10-131-827-2801	Sequence 2801, Ap	C 816	11.6	40.0	20	9	US-09-945-952A-8	Sequence 71, Appl
C 744	11.8	40.7	50	15	US-10-131-827-5914	Sequence 5914, Ap	C 817	11.6	40.0	20	10	US-09-793-807-71	Sequence 78, Appl
C 745	11.8	40.7	52	14	US-10-103-349A-33	Sequence 33, Appl	C 818	11.6	40.0	20	14	US-10-008-789-78	Sequence 8, Appl
			53	13	US-10-041-007-40	Sequence 40, Appl							

819	11.6	40.0	20	14	US-10-233-942-39	Sequence 39, Appl	31	10	US-09-817-879-7644	Sequence 7644, Ap
C 820	11.6	40.0	20	15	US-10-181-875-29	Sequence 29, Appl	31	10	US-09-817-879-8146	Sequence 8146, Ap
C 821	11.6	40.0	20	15	US-10-323-069A-57	Sequence 57, Appl	31	10	US-09-817-879-8595	Sequence 8595, Ap
C 822	11.6	40.0	20	15	US-10-159-856-21	Sequence 21, Appl	31	10	US-09-817-879-8641	Sequence 8641, Ap
C 823	11.6	40.0	20	15	US-10-159-856-95	Sequence 95, Appl	31	10	US-09-817-879-8705	Sequence 8705, Ap
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C 825	11.6	40.0	20	15	US-10-189-267-73	Sequence 73, Appl	31	10	US-09-817-879-8811	Sequence 8811, Ap
C 826	11.6	40.0	21	9	US-09-402-100-42	Sequence 42, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 827	11.6	40.0	21	9	US-10-349-143-10520	Sequence 10520, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 828	11.6	40.0	22	9	US-09-969-373-3564	Sequence 3564, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 829	11.6	40.0	24	10	US-09-850-514-27	Sequence 27, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 830	11.6	40.0	24	10	US-09-839-478-25	Sequence 25, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
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C 832	11.6	40.0	25	14	US-10-215-112-2021	Sequence 2021, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 833	11.6	40.0	25	14	US-10-215-112-591	Sequence 591, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 834	11.6	40.0	25	14	US-10-215-112-5917	Sequence 5917, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 835	11.6	40.0	25	14	US-10-215-112-11311	Sequence 11311, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 836	11.6	40.0	25	14	US-10-098-263B-5191	Sequence 5191, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 837	11.6	40.0	25	14	US-10-098-263B-13112	Sequence 13112, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 838	11.6	40.0	25	14	US-10-098-263B-32657	Sequence 32657, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 839	11.6	40.0	25	14	US-10-098-263B-37315	Sequence 37315, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 840	11.6	40.0	25	14	US-10-098-263B-41776	Sequence 41776, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 841	11.6	40.0	25	14	US-10-098-263B-45873	Sequence 45873, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 842	11.6	40.0	25	14	US-10-098-263B-63715	Sequence 63715, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 843	11.6	40.0	25	14	US-10-098-263B-64674	Sequence 64674, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 844	11.6	40.0	25	14	US-10-098-263B-70412	Sequence 70412, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 845	11.6	40.0	25	14	US-10-098-263B-70669	Sequence 70669, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 846	11.6	40.0	25	14	US-10-098-263B-75802	Sequence 75802, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 847	11.6	40.0	25	14	US-10-098-263B-85479	Sequence 85479, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 848	11.6	40.0	25	14	US-10-098-263B-92355	Sequence 92355, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 849	11.6	40.0	25	14	US-10-098-263B-104391	Sequence 104391, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 850	11.6	40.0	25	14	US-10-098-263B-104430	Sequence 104430, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 851	11.6	40.0	25	14	US-10-098-263B-105017	Sequence 105017, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 852	11.6	40.0	25	14	US-10-098-263B-105074	Sequence 105074, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 853	11.6	40.0	25	14	US-10-098-263B-117078	Sequence 117078, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 854	11.6	40.0	25	14	US-10-098-263B-128196	Sequence 128196, A	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 855	11.6	40.0	26	14	US-10-251-115-32	Sequence 32, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 856	11.6	40.0	26	14	US-10-170-221-5	Sequence 5, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 857	11.6	40.0	26	14	US-10-170-221-12	Sequence 12, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 858	11.6	40.0	27	9	US-09-789-657A-4	Sequence 4, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 859	11.6	40.0	27	9	US-10-233-996-21	Sequence 21, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 860	11.6	40.0	28	15	US-10-131-827-8910	Sequence 8910, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 861	11.6	40.0	28	15	US-10-131-827-8911	Sequence 8911, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 862	11.6	40.0	29	14	US-10-345-092-81	Sequence 81, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 863	11.6	40.0	29	14	US-10-336-638-345	Sequence 345, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 864	11.6	40.0	30	9	US-09-937-832-21	Sequence 21, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 865	11.6	40.0	30	12	US-10-352-155-405	Sequence 405, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 866	11.6	40.0	30	12	US-10-352-155-406	Sequence 406, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 867	11.6	40.0	31	9	US-09-771-043-1	Sequence 1, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 868	11.6	40.0	31	9	US-09-907-574-16	Sequence 16, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 869	11.6	40.0	31	9	US-09-068-528B-16	Sequence 16, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 870	11.6	40.0	31	9	US-09-736-084-35	Sequence 35, Appl	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 871	11.6	40.0	31	10	US-09-730-289B-2989	Sequence 2989, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 872	11.6	40.0	31	10	US-09-780-533A-5410	Sequence 5410, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 873	11.6	40.0	31	10	US-09-877-478-4679	Sequence 4679, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 874	11.6	40.0	31	10	US-09-848-754A-6580	Sequence 6580, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 875	11.6	40.0	31	10	US-09-848-754A-6580	Sequence 6580, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 876	11.6	40.0	31	10	US-09-776-474-2236	Sequence 2236, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 877	11.6	40.0	31	10	US-09-930-423-3576	Sequence 3576, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 878	11.6	40.0	31	10	US-09-740-332-7974	Sequence 7974, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 879	11.6	40.0	31	10	US-09-740-332-7974	Sequence 7974, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 880	11.6	40.0	31	10	US-09-740-332-7551	Sequence 7551, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 881	11.6	40.0	31	10	US-09-740-332-7644	Sequence 7644, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 882	11.6	40.0	31	10	US-09-740-332-8146	Sequence 8146, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 883	11.6	40.0	31	10	US-09-740-332-8595	Sequence 8595, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 884	11.6	40.0	31	10	US-09-740-332-8641	Sequence 8641, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 885	11.6	40.0	31	10	US-09-740-332-8705	Sequence 8705, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 886	11.6	40.0	31	10	US-09-740-332-8811	Sequence 8811, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 887	11.6	40.0	31	10	US-09-745-237A-3576	Sequence 3576, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 888	11.6	40.0	31	10	US-09-817-879-5794	Sequence 5794, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 889	11.6	40.0	31	10	US-09-817-879-7097	Sequence 7097, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 890	11.6	40.0	31	10	US-09-817-879-7551	Sequence 7551, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap
C 891	11.6	40.0	31	10	US-09-817-879-7551	Sequence 7551, Ap	31	12	US-09-342-902-4679	Sequence 4679, Ap


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; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 18-LIB34-011-Q1-E1-E5
US-09-983-965-4754

Query Match      53.1%; Score 15.4; DB 9; Length 53;
Best Local Similarity 44.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 5 AUUCUUUUGUAGCCCAAGGCGCU 29
Db 28 ATTCTTGTGTTGCCCTCAGGCT 52

RESULT 4
US-10-349-143-1097
; Sequence 1097, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1097
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2043-220 : polymorphic base A or T
US-10-349-143-1097

Query Match      52.4%; Score 15.2; DB 15; Length 47;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGAUUUUUUUGUAGCCCAAA 24
Db 15 AGACTCTTGTGTAACCTCCA 36

RESULT 5
US-09-908-975-18725/c
; Sequence 18725, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
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; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18725
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18725

Query Match      52.4%; Score 15.2; DB 10; Length 60;
Best Local Similarity 60.0%; Pred. No. 4.6e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 7 UCUUUUUUGUAGCCCAAGG 26
Db 26 TCTTCTGAAAGCCCATGG 7

RESULT 6
US-10-116-519-18
; Sequence 18, Application US/10116519
; Publication No. US20030114373A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN
; FILE REFERENCE: D0124 NP
; CURRENT APPLICATION NUMBER: US/10/116,519
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/281,253
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/288,768
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/296,180
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/300,620
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-519-18

Query Match      51.7%; Score 15; DB 14; Length 39;
Best Local Similarity 56.5%; Pred. No. 5.1e+03;
Matches 13; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GAUUCUUUUUUGUAGCCCAAGG 26
Db 5 GGTTCCTTCTGAAAGCTCAAGG 27

RESULT 7
US-09-908-975-12187/c
; Sequence 12187, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
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; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 12187
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12187

Query Match          51.7%; Score 15; DB 10; Length 60;
Best Local Similarity 47.8%; Pred. No. 5.6e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 AGAUUUUUUUUAAGCCCAAG 25
    |||:::|::|::|::|
Db 55 AGATTCTTCTGTAGCCGTAAG 33

RESULT 8
US-09-908-975-4580
; Sequence 4580, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4580
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-4580

Query Match          51.7%; Score 15; DB 10; Length 65;
Best Local Similarity 56.5%; Pred. No. 5.7e+03;
Matches 13; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUUUAAGCCCAAA 24
    |||:::|::|::|::|
Db 34 AAGATGCTTCTGTGAAGCAACA 56

RESULT 9
US-09-839-478-31/c
; Sequence 31, Application US/09839478
; Publication No. US20030180724A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; APPLICANT: Lins, Ann M.
; TITLE OF INVENTION: MULTIPLEX AMPLIFICATION OF SHORT TANDEM
; REPEAT LOCI
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: P. O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,478
; FILING DATE: 20-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,544
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-839-478-31

Query Match          51.0%; Score 14.8; DB 10; Length 29;
Best Local Similarity 42.3%; Pred. No. 5.9e+03;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUAAGCCCAAGGGCU 29
    |||:::|::|::|::|
Db 29 GATTATCTTTCATCCACTAGGGCT 4

RESULT 10
US-10-005-530-18
; Sequence 18, Application US/10005530
; Publication No. US20030026795A1
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING INSECTS
; FILE REFERENCE: 11899.0022.DVUS01 (MOBT:022--2)
; CURRENT APPLICATION NUMBER: US/10/005,530
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 09/063,733
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/044,504
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-005-530-18

Query Match          50.3%; Score 14.6; DB 14; Length 25;
Best Local Similarity 47.6%; Pred. No. 7.1e+03;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUUUAAGCCCC 22
    |||:::|::|::|::|
Db 5 AAGCTTCCTCTTGTAATACCC 25

RESULT 11
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US-09-908-975-8435
; Sequence 8435, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36898-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8435
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-8435

Query Match          50.3%; Score 14.6; DB 10; Length 60;
Best Local Similarity 51.7%; Pred. No. 8.6e+03;
Matches 15; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAAGAUCUUCUUUGUAGCCCAAGGCU 29
DB 12 AACGAACCTGATGTAATCCCAAGGATCT 40

RESULT 12
US-09-908-975-18114
; Sequence 18114, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36898-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18114
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18114

Query Match          50.3%; Score 14.6; DB 10; Length 60;
Best Local Similarity 52.4%; Pred. No. 8.6e+03;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 9 UUUUUGUAGCCCAAGGCU 29
DB 7 TATTCTGAGTCCCAAGGCT 27

RESULT 13
US-10-378-094-45
; Sequence 45, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide encoding peptide with EPO activity
US-10-378-094-45

Query Match          50.3%; Score 14.6; DB 15; Length 60;
Best Local Similarity 52.4%; Pred. No. 8.6e+03;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UUCUUUUGUAGCCCAAGG 26
DB 36 TTGGTTTGATGCCCAAGG 56

RESULT 14
US-10-231-494-24
; Sequence 24, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(60)
US-10-231-494-24

Query Match          50.3%; Score 14.6; DB 16; Length 60;
Best Local Similarity 52.4%; Pred. No. 8.6e+03;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UUCUUUUGUAGCCCAAGG 26
DB 36 TTGGTTTGATGCCCAAGG 56
```

RESULT 15

US-09-864-761-23841/c
; Sequence 23841, Application US/09864761
; Patent NO. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Shairon G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23841
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC01111.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
; OTHER INFORMATION: NT HIT: G14506086, EVALUATE 9.10e+00
; OTHER INFORMATION: EST_HUMAN HIT: BES42663.1, EVALUATE 5.60e-02
US-09-864-761-23841
Query Match 50.3%; Score 14.6; DB 9; Length 75;
Best Local Similarity 48.3%; Pred. No. 9e+03;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

RESULT 16

US-09-848-754A-6937/c
; Sequence 6937, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6937
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-6937
Query Match 49.7%; Score 14.4; DB 10; Length 31;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 17

US-09-740-332-5660/c
; Sequence 5660, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme
US-09-740-332-5660
Query Match 49.7%; Score 14.4; DB 10; Length 31;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 18

US-09-817-879-5660/c
; Sequence 5660, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MEHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme
; US-09-817-879-5660

Query Match          49.7%; Score 14.4; DB 10; Length 31;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY  2 AAGAUUUUUUUUAAGCCCAAG 25
    |||||: : : |||||
Db   27 AAGATCGTTGTAGTACGCCCAAG 4

RESULT 19
US-09-908-975-3924/c
; Sequence 3924, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3924
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-908-975-3924

Query Match          49.7%; Score 14.4; DB 10; Length 65;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY  1 AAGAUUUUUUUUAAGCCCAAG 24
    |||||: : : |||||
Db   35 AGAGATTCCTTTGTGAAGCGTAA 12

RESULT 20
US-09-975-30555
; Sequence 30555, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
```

```
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30555
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-908-975-30555

Query Match          49.7%; Score 14.4; DB 10; Length 65;
Best Local Similarity 54.2%; Pred. No. 1.1e+04;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY  5 AUUCUUUUUUUAAGCCCAAGGC 28
    |||||: : : |||||
Db   32 ATTCTGTGTGAAGCCCACTGC 55

RESULT 21
US-09-827-998-1098/c
; Sequence 1098, Application US/09827998
; Patent No. US2002010252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acemica Sequence Listing Engine
; SEQ ID NO 1098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-1098

Query Match          49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY  7 UCUUUUUUUAAGCCCAAG 25
    |||||: : : |||||
Db   25 TCTTTTGTAGTCCCTAAG 7

RESULT 22
US-09-827-998-1099/c
; Sequence 1099, Application US/09827998
; Patent No. US2002010252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
```

; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1099
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-1099

Query Match 49.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 47.4%; Pred. No. 1.1e+04;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUIUUUGUAGCCCAAG 25
 Db 24 TCTTTTGTAGTCCCTAAG 6

RESULT 23

US-09-827-998-1100/c
 ; Sequence 1100, Application US/09827998
 ; Patent No. US20020102252A1
 ; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: MDMORF-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; CURRENT FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1100
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-1100

Query Match 49.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 47.4%; Pred. No. 1.1e+04;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUIUUUGUAGCCCAAG 25
 Db 23 TCTTTTGTAGTCCCTAAG 5

RESULT 24

US-09-827-998-1101/c
 ; Sequence 1101, Application US/09827998
 ; Patent No. US20020102252A1
 ; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: MDMORF-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; CURRENT FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1101
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-1101

Query Match 49.0%; Score 14.2; DB 9; Length 25;

Best Local Similarity 47.4%; Pred. No. 1.1e+04;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUIUUUGUAGCCCAAG 25
 Db 22 TCTTTTGTAGTCCCTAAG 4

RESULT 25

US-09-827-998-1102/c
 ; Sequence 1102, Application US/09827998
 ; Patent No. US20020102252A1
 ; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: MDMORF-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; CURRENT FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1102
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-1102

Query Match 49.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 47.4%; Pred. No. 1.1e+04;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUIUUUGUAGCCCAAG 25
 Db 21 TCTTTTGTAGTCCCTAAG 3

RESULT 26

US-09-827-998-1103/c
 ; Sequence 1103, Application US/09827998
 ; Patent No. US20020102252A1
 ; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: MDMORF-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; CURRENT FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1103
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-1103

Query Match 49.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 47.4%; Pred. No. 1.1e+04;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUIUUUGUAGCCCAAG 25
 Db 20 TCTTTTGTAGTCCCTAAG 2

RESULT 27

```
US-09-827-998-1104/c
; Sequence 1104, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1104

Query Match          49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAAGCCCAAG 25
DB 19 TCTTTTGTAGTCCCTAAG 1

RESULT 28
US-10-675-685-1098/c
; Sequence 1098, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1098

Query Match          49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAAGCCCAAG 25
DB 25 TCTTTTGTAGTCCCTAAG 7

RESULT 29
US-10-675-685-1099/c
; Sequence 1099, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685

US-09-827-998-1104/c
; Sequence 1104, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1100/c
; Sequence 1100, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1100

Query Match          49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAAGCCCAAG 25
DB 23 TCTTTTGTAGTCCCTAAG 5

RESULT 31
US-10-675-685-1101/c
; Sequence 1101, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1101
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1101

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25
Db 22 TCTTTTGTAGTCCCTAAG 4

RESULT 32
US-10-675-685-1102/c
; Sequence 1102, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1102

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25
Db 21 TCTTTTGTAGTCCCTAAG 3

RESULT 33
US-10-675-685-1103/c
; Sequence 1103, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1103

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1104/c
; Sequence 1104, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1104

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25
Db 19 TCTTTTGTAGTCCCTAAG 1

RESULT 35
US-10-098-263B-76444
; Sequence 76444, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76444
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-76444

Query Match      49.0%; Score 14.2; DB 14; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAUUCUUUUGUAGCCCC 22
Db 1 GATACCTTTTAAAGTCCC 19

RESULT 36
US-10-287-919-545
; Sequence 545, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
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; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 545
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (143613)...(143638)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 638
US-10-287-919-545

Query Match      49.0%; Score 14.2; DB 14; Length 26;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 11 UUUUUAAGCCCAAGGCGU 29
Db 2 TTTAGAGCCCAAGGCGT 20

RESULT 37
US-09-848-754A-6794/c
; Sequence 6794, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6794
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-848-754A-6794

Query Match      49.0%; Score 14.2; DB 10; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 AAGAUUCUUUUUUAAGCCCAAGGCG 28
Db 27 AAGTCGTTGTAGCTAGCCCAAGGCG 1

RESULT 38
US-09-740-332-7606/c
; Sequence 7606, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7606
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme

US-09-740-332-7606

Query Match      49.0%; Score 14.2; DB 10; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUUUAAGCCCAAGGG 27
Db 28 AAAGATCGTTGTAGCTAGCCCTCCAGGG 2

RESULT 39
US-09-817-879-7606/c
; Sequence 7606, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7606
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme

US-09-817-879-7606

Query Match      49.0%; Score 14.2; DB 10; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUUUAAGCCCAAGGG 27
Db 28 AAAGATCGTTGTAGCTAGCCCTCCAGGG 2

RESULT 40
US-09-927-046-4415/c
; Sequence 4415, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channels
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4415
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-927-046-4415

Query Match      49.0%; Score 14.2; DB 12; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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Tue Apr 20 10:03:05 2004

QY 2 AAGAUUUUUUUUAAGCCCCAAGGC 28
Db : : : : :
27 AATATCGTTGTAGCTAGCCCCCTAGGC 1

Search completed: April 18, 2004, 11:55:33
Job time : 166.667 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:09:18 ; Search time 746.333 Seconds
(without alignments)
1684.164 Million cell updates/sec

Title: US-09-310-844C-24

Perfect score: 29

Sequence: 1 uaucauuuuuuuuaagccuuaggggcu 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1774092

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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2: gb.hsg.*

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32: em.htg.mus.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

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40: em.htgo.mus.*

41: em.htgo.Other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	28	96.6	46	6	BD274252	Identific
6	28	96.6	46	6	BD274253	Identific
7	28	96.6	46	6	BD274257	Identific
8	28	96.6	46	6	BD274265	Identific
9	28	96.6	46	6	BD274268	Identific
10	28	96.6	46	6	BD274269	Identific
11	25.8	89.0	42	6	BD274270	Identific
12	25.8	89.0	42	6	BD274278	Identific
13	24.8	85.5	46	6	BD274238	Identific
14	24.8	85.5	46	6	BD274236	Identific
15	23.8	82.1	42	6	BD274271	Identific
16	23.8	82.1	42	6	BD274279	Identific
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19	23.2	80.0	42	6	BD274272	Identific
20	23.2	80.0	42	6	BD274273	Identific
21	23.2	80.0	42	6	BD274280	Identific
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23	22.6	77.9	46	6	BD274284	Identific
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25	22.2	76.6	46	6	BD274242	Identific
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29	22.2	76.6	46	6	BD274260	Identific
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38	19.4	66.9	46	6	BD274257	Identific
39	18.4	63.4	42	6	BD274274	Identific
40	18.4	63.4	42	6	BD274282	Identific
41	18	62.1	44	6	BD274277	Identific
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44	15.4	53.1	41	6	AX520728	Sequence
45	15.2	52.4	33	6	AR020509	Sequence
46	15	51.7	40	6	E49126	Novel G pro
47	15	51.7	40	6	E50836	Novel G pro
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49	14.8	51.0	35	6	AR364722	Sequence
50	14.8	51.0	36	6	AR142180	Sequence
51	14.8	51.0	43	6	AX483394	Sequence
52	14.6	50.3	51	6	AX115517	Sequence
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54	14.6	50.3	53	9	S63972	IGH (CD3 z
55	14.6	50.3	55	6	AX484927	Sequence
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61	14.2	49.0	25	6	AR434677	Sequence
62	14.2	49.0	25	6	AR434678	Sequence
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C 68	14.2	49.0	42	6	BD274273	Identific	141	13.4	46.2	42	6	BD003417	Soluble p
C 69	14.2	49.0	42	6	BD274280	Identific	142	13.4	46.2	43	8	ATH553793	Arabidops
C 70	14.2	49.0	42	6	BD274281	Identific	143	13.4	46.2	47	6	AX194666	Sequence
C 71	14.2	49.0	45	6	I04390	Sequence 25	C 144	13.4	46.2	47	6	AX378367	Sequence
C 72	14.2	49.0	45	6	AX923415	Sequence	C 145	13.4	46.2	49	3	DD063607	Dictyosteli
C 73	14.2	49.0	50	6	AX781523	Sequence	C 146	13.4	46.2	51	6	E2819	PCR primer
C 74	14.2	49.0	51	6	AX817032	Sequence	C 147	13.4	46.2	51	6	I26179	Sequence 11
C 75	14.2	49.0	56	6	AX247478	Sequence	C 148	13.4	46.2	52	6	BD270556	Family of
C 76	14.2	49.0	56	6	AX256904	Sequence	C 149	13.4	46.2	52	6	AR208953	Sequence
C 77	14.2	49.0	30	6	AR256906	Sequence	C 150	13.4	46.2	52	6	AR228346	Sequence
C 78	14.2	49.0	30	6	AX113961	Sequence	C 151	13.4	46.2	52	6	AX046943	Sequence
C 79	14.2	49.0	30	6	AX113963	Sequence	C 152	13.4	46.2	52	6	AX428345	Sequence
C 80	14.2	49.0	37	6	AR003420	Sequence	C 153	13.4	46.2	52	6	BD082716	Family of
C 81	14.2	49.0	37	6	I21209	Sequence 55	C 154	13.4	46.2	54	6	AX404651	Sequence
C 82	14.2	49.0	37	6	I74476	Sequence 55	C 155	13.4	46.2	56	6	AX523133	Sequence
C 83	14.2	49.0	37	6	AX555864	Sequence	C 156	13.4	46.2	57	8	AX591789	Arabidops
C 84	14.2	49.0	37	6	AX555865	Sequence	C 157	13.4	46.2	60	6	AR254137	Sequence
C 85	14.2	49.0	44	6	AR003419	Sequence	C 158	13.4	46.2	60	8	AX596988	Arabidops
C 86	14.2	49.0	44	6	I21208	Sequence 54	C 159	13.4	46.2	61	14	ALRBS616	Rous sarcom
C 87	14.2	49.0	44	6	I74475	Sequence 54	C 160	13.4	46.2	65	6	AX484878	Sequence
C 88	14.2	49.0	55	8	AX598912	Arabidops	C 161	13.4	46.2	77	8	SPO222770	Schizosac
C 89	14.2	49.0	60	6	AX676039	Sequence	C 162	13.2	45.5	25	6	AR434674	Sequence
C 90	14.2	49.0	62	6	AX899399	Sequence	C 163	13.2	45.5	26	8	ATH529956	Arabidops
C 91	14.2	49.0	62	6	BD034932	Sequence	C 164	13.2	45.5	27	6	BD230947	49 human
C 92	14.2	49.0	78	14	AF362846	HIV-1 iso	C 165	13.2	45.5	27	6	BD231661	31 human
C 93	14.2	49.0	78	14	AF362847	HIV-1 iso	C 166	13.2	45.5	27	6	BD233712	31 human
C 94	14.2	49.0	78	14	AF362849	HIV-1 iso	C 167	13.2	45.5	27	6	BD243600	TNFR rela
C 95	13.8	47.6	17	6	AR433860	Sequence	C 168	13.2	45.5	27	6	BD243606	BD243606
C 96	13.8	47.6	25	6	AR434682	Sequence	C 169	13.2	45.5	27	6	BD248833	47 human
C 97	13.8	47.6	25	6	AR434683	Sequence	C 170	13.2	45.5	27	6	BD249071	49 human
C 98	13.8	47.6	25	6	AX527257	Sequence	C 171	13.2	45.5	27	6	BD249129	27 human
C 99	13.8	47.6	31	6	AX426018	Sequence	C 172	13.2	45.5	27	6	BD249183	48 human
C 100	13.8	47.6	36	6	AR142182	Sequence	C 173	13.2	45.5	27	6	BD249801	33 human
C 101	13.8	47.6	42	6	AX017119	Sequence	C 174	13.2	45.5	27	6	BD249894	50 human
C 102	13.8	47.6	42	6	AX017120	Sequence	C 175	13.2	45.5	27	6	BD249953	50 human
C 103	13.8	47.6	42	6	AX017120	Sequence	C 176	13.2	45.5	27	6	BD250041	48 human
C 104	13.8	47.6	50	6	AR288904	Sequence	C 177	13.2	45.5	27	6	BD250098	49 human
C 105	13.8	47.6	50	6	AX157596	Sequence	C 178	13.2	45.5	27	6	BD250169	45 human
C 106	13.8	47.6	50	6	AX164867	Sequence	C 179	13.2	45.5	27	6	BD250169	45 human
C 107	13.8	47.6	59	10	CRUDELFNF	M27128 Chinese Ham	C 180	13.2	45.5	27	6	BD252043	47 secret
C 108	13.8	47.6	65	6	AX482858	Sequence	C 181	13.2	45.5	27	6	BD260155	50 human
C 109	13.8	47.6	79	6	AX914035	Sequence	C 182	13.2	45.5	27	6	BD260603	49 human
C 110	13.8	47.6	79	6	BD049568	Sequence	C 183	13.2	45.5	27	6	BD260661	50 human
C 111	13.6	46.9	25	6	AX610026	Sequence	C 184	13.2	45.5	27	6	BD260720	50 human
C 112	13.6	46.9	25	6	AX610027	Sequence	C 185	13.2	45.5	27	6	BD260786	50 human
C 113	13.6	46.9	31	6	AX223552	Sequence	C 186	13.2	45.5	27	6	BD260940	Galectin
C 114	13.6	46.9	31	6	AX249149	Sequence	C 187	13.2	45.5	27	6	BD260946	Galectin
C 115	13.6	46.9	37	6	AX183756	Sequence	C 188	13.2	45.5	27	6	BD264592	12 human
C 116	13.6	46.9	40	6	AX456426	Sequence	C 189	13.2	45.5	27	6	BD266680	Prostacyc
C 117	13.6	46.9	42	6	AR264216	Sequence	C 190	13.2	45.5	27	6	BD266910	29 human
C 118	13.6	46.9	44	6	A36495	Sequence 36	C 191	13.2	45.5	27	6	BD266916	Bone marr
C 119	13.6	46.9	44	6	AR080128	Sequence	C 192	13.2	45.5	27	6	BD269268	33 human
C 120	13.6	46.9	47	6	AR290551	Sequence	C 193	13.2	45.5	27	6	BD269733	30 human
C 121	13.6	46.9	50	6	AX160546	Sequence	C 194	13.2	45.5	27	6	BD270314	50 human
C 122	13.6	46.9	51	6	AX160545	Sequence	C 195	13.2	45.5	27	6	BD270384	49 human
C 123	13.6	46.9	51	6	AX160547	Sequence	C 196	13.2	45.5	27	6	BD271538	49 human
C 124	13.6	46.9	51	6	AX498444	Sequence	C 197	13.2	45.5	27	6	BD275003	50 human
C 125	13.6	46.9	55	6	AR358906	Sequence	C 198	13.2	45.5	27	6	BD275062	47 human
C 126	13.6	46.9	68	1	AF178301S1	Chlamydia	C 199	13.2	45.5	27	6	BD275124	48 human
C 127	13.6	46.9	68	1	LAWREN10	KO3314 Bacterioph	C 200	13.2	45.5	27	6	BD275181	46 human
C 128	13.4	46.2	25	6	AX043007	Sequence	C 201	13.2	45.5	27	6	BD275270	48 human
C 129	13.4	46.2	26	6	BD238414	Sorting o	C 202	13.2	45.5	27	6	BD275327	49 human
C 130	13.4	46.2	26	6	AR431395	Sequence	C 203	13.2	45.5	27	6	BD275386	50 human
C 131	13.4	46.2	26	6	AX055927	Sequence	C 204	13.2	45.5	27	6	BD275445	47 human
C 132	13.4	46.2	26	6	BD190535	Method fo	C 205	13.2	45.5	27	6	BD275501	48 human
C 133	13.4	46.2	30	6	AX790896	Sequence	C 206	13.2	45.5	27	6	BD275925	62 human
C 134	13.4	46.2	31	6	AX426127	Sequence	C 207	13.2	45.5	27	6	BD276018	48 human
C 135	13.4	46.2	35	6	AX367005	Sequence	C 208	13.2	45.5	27	6	BD276331	143 human
C 136	13.4	46.2	38	6	BD170439	Transgeni	C 209	13.2	45.5	27	6	AR184060	Sequence
C 137	13.4	46.2	41	6	AR049546	Sequence	C 210	13.2	45.5	27	6	AR203345	Sequence
C 138	13.4	46.2	41	6	AR065751	Sequence	C 211	13.2	45.5	27	6	AR206967	Sequence

212	13.2	45.5	27	6	AR216179	Sequence	AR216179	Sequence	C 285	13.2	45.5	42	8	AJ595838	Arabidops
213	13.2	45.5	27	6	AR229178	Sequence	AR229178	Sequence	286	13.2	45.5	47	6	AR291107	Sequence
214	13.2	45.5	27	6	AR242462	Sequence	AR242462	Sequence	287	13.2	45.5	51	6	AX117185	Sequence
215	13.2	45.5	27	6	AR243034	Sequence	AR243034	Sequence	288	13.2	45.5	65	6	AX463337	Sequence
216	13.2	45.5	27	6	AR243766	Sequence	AR243766	Sequence	289	13.2	45.5	66	1	S66739	ompl-major
217	13.2	45.5	27	6	AR257348	Sequence	AR257348	Sequence	290	13.2	45.5	76	6	AX593379	Sequence
218	13.2	45.5	27	6	AR257354	Sequence	AR257354	Sequence	291	13.2	45.5	76	8	AJ598293	Arabidops
219	13.2	45.5	27	6	AR271236	Sequence	AR271236	Sequence	292	13	44.8	24	6	AR224221	Sequence
220	13.2	45.5	27	6	AR271242	Sequence	AR271242	Sequence	293	13	44.8	25	6	AX042933	Sequence
221	13.2	45.5	27	6	AR275686	Sequence	AR275686	Sequence	294	13	44.8	25	6	AX043321	Sequence
222	13.2	45.5	27	6	AR275692	Sequence	AR275692	Sequence	295	13	44.8	25	6	AX116440	Sequence
223	13.2	45.5	27	6	AR337242	Sequence	AR337242	Sequence	296	13	44.8	25	6	AX448011	Sequence
224	13.2	45.5	27	6	AR339743	Sequence	AR339743	Sequence	297	13	44.8	33	6	E15490	Primer. 7/1
225	13.2	45.5	27	6	AR352597	Sequence	AR352597	Sequence	298	13	44.8	38	6	AX219881	Sequence
226	13.2	45.5	27	6	AR353859	Sequence	AR353859	Sequence	299	13	44.8	41	6	AX514585	Sequence
227	13.2	45.5	27	6	AR374485	Sequence	AR374485	Sequence	300	13	44.8	41	6	AX518045	Sequence
228	13.2	45.5	27	6	AR374704	Sequence	AR374704	Sequence	301	13	44.8	41	6	AX520024	Sequence
229	13.2	45.5	27	6	AR374925	Sequence	AR374925	Sequence	302	13	44.8	48	6	AX018731	Sequence
230	13.2	45.5	27	6	AR374931	Sequence	AR374931	Sequence	303	13	44.8	49	6	AR219989	Sequence
231	13.2	45.5	27	6	AR399699	Sequence	AR399699	Sequence	304	13	44.8	51	6	AX116441	Sequence
232	13.2	45.5	27	6	AR404215	Sequence	AR404215	Sequence	305	13	44.8	51	6	AX157944	Sequence
233	13.2	45.5	27	6	AR409272	Sequence	AR409272	Sequence	306	13	44.8	51	6	AX781524	Sequence
234	13.2	45.5	27	6	AX676269	Sequence	AX676269	Sequence	307	13	44.8	51	6	AX817033	Sequence
235	13.2	45.5	27	6	AX676275	Sequence	AX676275	Sequence	308	13	44.8	51	10	AF094484	AF094484 Mus muscu
236	13.2	45.5	27	6	AX810680	Sequence	AX810680	Sequence	309	13	44.8	51	10	AF205733	AF205733 Mus muscu
237	13.2	45.5	27	6	AX815061	Sequence	AX815061	Sequence	310	13	44.8	51	10	AF205745	AF205745 Mus muscu
238	13.2	45.5	27	6	AX839498	Sequence	AX839498	Sequence	311	13	44.8	53	6	AR061021	AR061021 Sequence
239	13.2	45.5	27	6	BD072942	70 human	BD072942	70 human	312	13	44.8	53	6	AR147183	AR147183 Sequence
240	13.2	45.5	27	6	BD074288	50 human	BD074288	50 human	313	13	44.8	53	6	BD083543	BD083543 The Nucca
241	13.2	45.5	27	6	BD074455	Human fri	BD074455	Human fri	314	13	44.8	53	10	MDTRVNB	X63580 M.domesticu
242	13.2	45.5	27	6	BD074461	Human fri	BD074461	Human fri	315	13	44.8	54	6	BD271077	BD271077 Method an
243	13.2	45.5	27	6	BD078076	Human tum	BD078076	Human tum	316	13	44.8	54	6	AR258483	AR258483 Sequence
244	13.2	45.5	27	6	BD078082	Human tum	BD078082	Human tum	317	13	44.8	54	6	AX494568	AX494568 Sequence
245	13.2	45.5	27	6	BD078335	53 human	BD078335	53 human	318	13	44.8	54	10	AY177438	AY177438 Mus muscu
246	13.2	45.5	27	6	BD078414	101 human	BD078414	101 human	319	13	44.8	54	10	AY177439	AY177439 Mus muscu
247	13.2	45.5	27	6	BD082361	87 human	BD082361	87 human	320	13	44.8	55	6	AR147184	AR147184 Sequence
248	13.2	45.5	27	6	BD082593	20 human	BD082593	20 human	321	13	44.8	55	6	BD083544	BD083544 The Nucca
249	13.2	45.5	27	6	BD084155	28 human	BD084155	28 human	322	13	44.8	57	6	I30325	I30325 Sequence 14
250	13.2	45.5	27	6	BD107832	36 human	BD107832	36 human	323	13	44.8	60	6	AX538259	AX538259 Sequence
251	13.2	45.5	27	6	BD124018	Dendritic	BD124018	Dendritic	324	13	44.8	62	6	AX049496	AX049496 Sequence
252	13.2	45.5	27	6	BD129620	Polynucle	BD129620	Polynucle	325	13	44.8	65	6	AX482910	AX482910 Sequence
253	13.2	45.5	27	6	BD129626	Polynucle	BD129626	Polynucle	326	13	44.8	65	6	AX483133	AX483133 Sequence
254	13.2	45.5	27	6	BD130945	67 human	BD130945	67 human	327	13	44.8	65	6	AX484875	AX484875 Sequence
255	13.2	45.5	27	6	BD131089	45 human	BD131089	45 human	328	13	44.8	65	6	AX486575	AX486575 Sequence
256	13.2	45.5	27	6	BD132834	Cardiotro	BD132834	Cardiotro	329	13	44.8	66	1	ECOHLETX	M17101 E.coli heat
257	13.2	45.5	27	6	BD132840	Cardiotro	BD132840	Cardiotro	330	13	44.8	70	6	AR123747	AR123747 Sequence
258	13.2	45.5	27	6	BD134709	31 human	BD134709	31 human	331	13	44.8	72	6	I25145	I25145 Sequence 41
259	13.2	45.5	27	6	BD135252	110 human	BD135252	110 human	332	13	44.8	73	6	AX090836	AX090836 Sequence
260	13.2	45.5	27	6	BD136316	95 human	BD136316	95 human	333	13	44.8	73	6	BD045369	BD045369 Sequence
261	13.2	45.5	27	6	BD137338	Cytokine	BD137338	Cytokine	334	13	44.8	77	6	AX092950	AX092950 Sequence
262	13.2	45.5	27	6	BD140617	36 human	BD140617	36 human	335	13	44.8	77	6	AX092951	AX092951 Sequence
263	13.2	45.5	27	6	BD191039	186 human	BD191039	186 human	336	13	44.8	77	6	AX167320	AX167320 Sequence
264	13.2	45.5	27	6	BD192080	32 human	BD192080	32 human	337	13	44.8	77	6	AX167321	AX167321 Sequence
265	13.2	45.5	27	6	BD192589	123 human	BD192589	123 human	338	13	44.8	77	6	AR048883	AR048883 Sequence
266	13.2	45.5	27	6	BD192909	207 human	BD192909	207 human	339	12.8	44.1	78	6	AR433859	AR433859 Sequence
267	13.2	45.5	27	6	BD194832	86 human	BD194832	86 human	340	12.8	44.1	17	6	AR433861	AR433861 Sequence
268	13.2	45.5	27	6	BD195542	70 human	BD195542	70 human	341	12.8	44.1	18	6	AR293731	AR293731 Sequence
269	13.2	45.5	27	6	BD203626	97 human	BD203626	97 human	342	12.8	44.1	20	6	AX056605	AX056605 Sequence
270	13.2	45.5	27	6	BD211207	Interleuk	BD211207	Interleuk	343	12.8	44.1	23	6	BD205443	BD205443 Recombina
271	13.2	45.5	27	6	BD211213	Interleuk	BD211213	Interleuk	344	12.8	44.1	24	6	I58350	I58350 Sequence 6
272	13.2	45.5	27	6	BD218522	71 human	BD218522	71 human	345	12.8	44.1	24	6	AR235262	AR235262 Sequence
273	13.2	45.5	27	6	BD222553	ETS facto	BD222553	ETS facto	346	12.8	44.1	24	6	AR285149	AR285149 Sequence
274	13.2	45.5	27	6	BD223068	98 human	BD223068	98 human	347	12.8	44.1	24	6	BD130249	BD130249 Member of
275	13.2	45.5	27	6	BD223400	94 human	BD223400	94 human	348	12.8	44.1	24	6	BD130339	BD130339 Member of
276	13.2	45.5	31	6	AX582468	Human	AX582468	Human	349	12.8	44.1	24	6	BD217680	BD217680 Choline a
277	13.2	45.5	31	6	AX582708	Sequence	AX582708	Sequence	350	12.8	44.1	25	6	AR434684	AR434684 Sequence
278	13.2	45.5	32	6	BD161922	Recombina	BD161922	Recombina	351	12.8	44.1	25	6	AX043250	AX043250 Sequence
279	13.2	45.5	35	11	C75983	C75983 Homo sapien	C75983	Homo sapien	352	12.8	44.1	25	6	AX527256	AX527256 Sequence
280	13.2	45.5	36	6	AR034089	Sequence	AR034089	Sequence	353	12.8	44.1	25	6	AX527258	AX527258 Sequence
281	13.2	45.5	36	6	AR071311	Sequence	AR071311	Sequence	354	12.8	44.1	25	6	AX616242	AX616242 Sequence
282	13.2	45.5	36	6	AR112727	Sequence	AR112727	Sequence	355	12.8	44.1	25	6	AX616243	AX616243 Sequence
283	13.2	45.5	40	6	BD107566	Nucleic a	BD107566	Nucleic a	356	12.8	44.1	26	6	AX195509	AX195509 Sequence
284	13.2	45.5	42	6	AX244233	Sequence	AX244233	Sequence	357	12.8	44.1	30	6	AX611431	AX611431 Sequence

C 358	12.8	44.1	30	6	AX791737	Sequence	C 431	12.6	43.4	29	6	I76812	Sequence 22
C 359	12.8	44.1	30	6	AX793354	Sequence	C 432	12.6	43.4	30	6	AX261297	Sequence
C 360	12.8	44.1	30	6	AX221037	Sequence	C 433	12.6	43.4	30	6	AX683638	Sequence
C 361	12.8	44.1	31	6	AX426065	Sequence	C 434	12.6	43.4	32	6	AR061867	Sequence
C 362	12.8	44.1	35	11	C75690	Homio sapien	C 435	12.6	43.4	32	6	BD233998	Multiple
C 363	12.8	44.1	38	6	AR048354	Sequence	C 436	12.6	43.4	32	6	AR252858	Sequence
C 364	12.8	44.1	38	6	I53406	Sequence 11	C 437	12.6	43.4	34	6	AR381466	Sequence
C 365	12.8	44.1	39	6	A26290	Subtilisin	C 438	12.6	43.4	34	6	AR381469	Sequence
C 366	12.8	44.1	39	6	A26922	oligonucleo	C 439	12.6	43.4	35	6	AX020426	Sequence
C 367	12.8	44.1	39	6	I43379	Sequence 8	C 440	12.6	43.4	36	6	I57363	Sequence 6
C 368	12.8	44.1	39	6	AR079795	Sequence	C 441	12.6	43.4	36	9	AF505540	Homio sapi
C 369	12.8	44.1	40	6	AR081325	Sequence	C 442	12.6	43.4	37	8	ATH552409	Arabidops
C 370	12.8	44.1	40	6	AR170685	Sequence	C 443	12.6	43.4	40	6	AX774088	Sequence
C 371	12.8	44.1	42	6	I86960	Sequence 49	C 444	12.6	43.4	41	6	AX519811	Sequence
C 372	12.8	44.1	45	6	AR032518	Sequence	C 445	12.6	43.4	42	6	BD274270	Identific
C 373	12.8	44.1	45	6	AR032730	Sequence	C 446	12.6	43.4	42	6	BD274278	Identific
C 374	12.8	44.1	45	6	I29258	Sequence 13	C 447	12.6	43.4	43	6	AS0152	Sequence 9
C 375	12.8	44.1	45	6	I29470	Sequence 34	C 448	12.6	43.4	44	6	BD274261	Identific
C 376	12.8	44.1	45	6	I90932	Sequence 13	C 449	12.6	43.4	45	6	AS1851	Sequence 15
C 377	12.8	44.1	45	6	I91144	Sequence 34	C 450	12.6	43.4	45	6	AR085824	Sequence
C 378	12.8	44.1	45	6	AR209182	Sequence	C 451	12.6	43.4	45	6	AX554059	Sequence
C 379	12.8	44.1	45	6	AR209394	Sequence	C 452	12.6	43.4	46	6	BD274245	Identific
C 380	12.8	44.1	47	6	AR288951	Sequence	C 453	12.6	43.4	47	6	AR288361	Sequence
C 381	12.8	44.1	47	6	AR289362	Sequence	C 454	12.6	43.4	50	6	AX164808	Sequence
C 382	12.8	44.1	48	14	SV4MNV1	K00807 simian viru	C 455	12.6	43.4	50	6	AX164809	Sequence
C 383	12.8	44.1	50	6	AR032731	Sequence	C 456	12.6	43.4	51	6	AX157595	Sequence
C 384	12.8	44.1	50	6	I29471	Sequence 34	C 457	12.6	43.4	51	6	AX190034	Sequence
C 385	12.8	44.1	50	6	I91145	Sequence 34	C 458	12.6	43.4	51	6	AX190035	Sequence
C 386	12.8	44.1	54	6	AR098551	Sequence	C 459	12.6	43.4	55	6	AR238787	Sequence
C 387	12.8	44.1	54	6	AR108893	Sequence	C 460	12.6	43.4	55	6	AX079194	Sequence
C 388	12.8	44.1	54	6	AR268150	Sequence	C 461	12.6	43.4	55	9	S65927	immunoglob
C 389	12.8	44.1	54	6	AR009660	Sequence	C 462	12.6	43.4	59	6	AX601370	Sequence
C 390	12.8	44.1	54	6	AR009650	Sequence	C 463	12.6	43.4	59	11	AX295121	Arabidops
C 391	12.8	44.1	54	6	AR010922	Sequence	C 464	12.6	43.4	61	8	AR241984	Sequence
C 392	12.8	44.1	57	9	AF011598	Homio sapi	C 465	12.6	43.4	61	8	AJ587776	Arabidops
C 393	12.8	44.1	58	6	I05513	Sequence 1	C 466	12.6	43.4	64	6	AR009650	Sequence
C 394	12.8	44.1	58	6	I09141	Sequence 1	C 467	12.6	43.4	65	6	AX483070	Sequence
C 395	12.8	44.1	59	8	AJ590671	Arabidops	C 468	12.6	43.4	65	6	AX484865	Sequence
C 396	12.8	44.1	59	8	AJ599452	Arabidops	C 469	12.6	43.4	66	10	AX485056	Sequence
C 397	12.8	44.1	63	6	I07555	Sequence 5	C 470	12.6	43.4	72	6	EO1872	DNA encodin
C 398	12.8	44.1	65	6	AX482799	Sequence	C 471	12.6	43.4	72	6	AX701724	Sequence
C 399	12.8	44.1	65	6	AX483243	Sequence	C 472	12.6	43.4	74	6	AX701724	Sequence
C 400	12.8	44.1	65	6	AX483283	Sequence	C 473	12.6	43.4	74	9	HUMAPOAG	Human apoli
C 401	12.8	44.1	65	6	AX483721	Sequence	C 474	12.6	43.4	78	8	ATH527607	Arabidops
C 402	12.8	44.1	65	6	AX483891	Sequence	C 475	12.6	43.4	79	14	MOXL	Mokola viru
C 403	12.8	44.1	65	6	AX484810	Sequence	C 476	12.6	43.4	80	6	AS1846	Sequence 10
C 404	12.8	44.1	66	8	AJ600346	Arabidops	C 477	12.6	43.4	80	6	AS1883	Sequence 47
C 405	12.8	44.1	67	8	AF136104	Ditrichum	C 478	12.6	43.4	80	6	AR085848	Sequence
C 406	12.8	44.1	68	6	AR356844	Sequence	C 479	12.6	43.4	80	11	AX294558	Arabidops
C 407	12.8	44.1	68	6	AX908830	Sequence	C 480	12.6	43.4	80	6	BD208934	Enzymatic
C 408	12.8	44.1	68	6	BD044363	Sequence	C 481	12.6	43.4	80	6	AR207325	Sequence
C 409	12.8	44.1	69	6	AX904939	Sequence	C 482	12.6	43.4	80	6	AR253153	Sequence
C 410	12.8	44.1	69	6	BD040472	Sequence	C 483	12.6	43.4	80	6	AR403671	Sequence
C 411	12.8	44.1	69	14	AF092639	HIV-1 pat	C 484	12.6	43.4	80	6	BD106724	Plasid P
C 412	12.8	44.1	75	8	ATH527247	Arabidops	C 485	12.6	43.4	80	6	AL16721	oligonucleo
C 413	12.8	44.1	77	6	A38260	Sequence 15	C 486	12.6	43.4	80	6	AR134911	Sequence
C 414	12.8	44.1	77	6	A38688	Sequence 15	C 487	12.6	43.4	80	6	AX042702	Sequence
C 415	12.8	44.1	77	6	AR101813	Sequence	C 488	12.6	43.4	80	6	AX042733	Sequence
C 416	12.8	44.1	79	6	AR155054	Sequence	C 489	12.6	43.4	80	6	AX042970	Sequence
C 417	12.8	44.1	79	8	AR156303	Sequence	C 490	12.6	43.4	80	6	AX043051	Sequence
C 418	12.8	44.1	79	8	OSA532510	Oryza sat	C 491	12.6	43.4	80	6	AX043512	Sequence
C 419	12.8	44.1	80	8	AJ593415	Arabidops	C 492	12.6	43.4	80	6	AX043553	Sequence
C 420	12.8	44.1	80	8	AJ593415	Arabidops	C 493	12.6	43.4	80	6	AX527259	Sequence
C 421	12.6	43.4	21	6	AX76928	Sequence	C 494	12.6	43.4	80	6	AX527260	Sequence
C 422	12.6	43.4	21	6	AX526304	Sequence	C 495	12.6	43.4	80	6	AR020775	Sequence
C 423	12.6	43.4	24	6	AX444982	Sequence	C 496	12.6	43.4	80	6	AR020755	Sequence
C 424	12.6	43.4	26	6	E22835	Promoter se	C 497	12.6	43.4	80	6	BD250380	Enzyme . 7
C 425	12.6	43.4	26	6	AX067180	Sequence	C 498	12.6	43.4	80	6	I34036	Sequence 10
C 426	12.6	43.4	26	6	BD177543	Method fo	C 499	12.6	43.4	80	6	I34052	Sequence 29
C 427	12.6	43.4	29	6	AR018900	Sequence	C 500	12.6	43.4	80	6	AX038769	Sequence
C 428	12.6	43.4	29	6	AR066528	Sequence	C 501	12.6	43.4	80	6	AR230012	Sequence
C 429	12.6	43.4	29	6	AR112066	Sequence	C 502	12.6	43.4	80	6	AX134143	Sequence
C 430	12.6	43.4	29	6	BD261033	Microbal	C 503	12.6	43.4	80	6		
			29	6	I72245	Sequence 22							

650	12.2	42.1	49	8	AJ599937	AJ599937 Arabidops	C 723	12	41.4	31	6	AR072430	AR072430 Sequence
C 651	12.2	42.1	51	6	A07731	A07731 Oligonucleo	C 724	12	41.4	31	6	126541	126541 Sequence
C 652	12.2	42.1	51	6	A10029	A10029 Nucleotide	C 725	12	41.4	31	6	AR342577	AR342577 Sequence
C 653	12.2	42.1	51	6	AR009025	AR009025 Sequence	C 726	12	41.4	31	6	AX425752	AX425752 Sequence
C 654	12.2	42.1	51	6	AR052680	AR052680 Sequence	C 727	12	41.4	31	6	AX582577	AX582577 Sequence
C 655	12.2	42.1	51	6	AR060991	AR060991 Sequence	C 728	12	41.4	33	6	AR119805	AR119805 Sequence
C 656	12.2	42.1	51	6	AR087722	AR087722 Sequence	C 729	12	41.4	33	6	BD243338	BD243338 Improved
C 657	12.2	42.1	51	6	AR175113	AR175113 Sequence	C 730	12	41.4	33	6	AR344239	AR344239 Sequence
C 658	12.2	42.1	51	6	AR287993	AR287993 Sequence	C 731	12	41.4	33	6	AR361666	AR361666 Sequence
C 659	12.2	42.1	51	6	AR287993	AR287993 Sequence	C 732	12	41.4	33	6	AX021816	AX021816 Sequence
C 660	12.2	42.1	51	6	AR360127	AR360127 Sequence	C 733	12	41.4	33	6	AX137248	AX137248 Sequence
C 661	12.2	42.1	51	6	AX115765	AX115765 Sequence	C 734	12	41.4	33	6	BD015172	BD015172 Continuo
C 662	12.2	42.1	51	6	AX157907	AX157907 Sequence	C 735	12	41.4	33	6	BD094291	BD094291 A prepara
C 663	12.2	42.1	51	6	AR261804	AR261804 Sequence	C 736	12	41.4	33	6	BD179370	BD179370 A novel p
C 664	12.2	42.1	54	6	AR268146	AR268146 Sequence	C 737	12	41.4	33	10	MDTRVJNK	X63559 M.domesticu
C 665	12.2	42.1	54	6	AX009656	AX009656 Sequence	C 738	12	41.4	34	6	AR225312	AR225312 Sequence
C 666	12.2	42.1	54	6	AX010918	AX010918 Sequence	C 739	12	41.4	34	6	BD062172	BD062172 Expresio
C 667	12.2	42.1	55	6	AF206138	AF206138 Rana chap	C 740	12	41.4	35	6	AX768186	AX768186 Sequence
C 668	12.2	42.1	55	6	AX484741	AX484741 Sequence	C 741	12	41.4	36	6	I36659	I36659 Sequence
C 669	12.2	42.1	56	6	AX9113897	AX9113897 Sequence	C 742	12	41.4	36	6	AR204491	AR204491 Sequence
C 670	12.2	42.1	57	6	BD049430	BD049430 Sequence	C 743	12	41.4	36	6	AR218089	AR218089 Sequence
C 671	12.2	42.1	57	6	AJ589198	AJ589198 Arabidops	C 744	12	41.4	36	6	AR230460	AR230460 Sequence
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C 673	12.2	42.1	60	6	AR116980	AR116980 Sequence	C 746	12	41.4	36	6	AR350567	AR350567 Sequence
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C 691	12.2	42.1	76	11	AL954623	AL954623 Arabidops	C 764	12	41.4	41	6	AR179776	AR179776 Sequence
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RESULT 3
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
ACCESSION BD274240
VERSION BD274240.1 GI:33084008
KEYWORDS JP 2002526030-A/207.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 207 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/207
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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RESULT 5
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
ACCESSION BD274252
VERSION BD274252.1 GI:33084020
KEYWORDS JP 2002526030-A/219.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 219 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Best Local Similarity 60.7%; Pred. No. 0.061;
Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUAUUCUUUUUGUAAGCCCUAGGGGC 28
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Db 19 TATGATTCCTTTTGTAAAGCCCTAGGGGC 46

RESULT 6
BD274253
LOCUS BD274253 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
ACCESSION BD274253
VERSION BD274253.1 GI:33084021
KEYWORDS JP 2002526030-A/220.

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[illegible]

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FEATURES             source
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/mol_type="genomic RNA"
/db_xref="taxon:32630"

ORIGIN
Query Match          96.6%;   Score 28;   DB 6;   Length 46;
Best Local Similarity 60.7%;   Pred.No. 0.061;
Matches 17;   Conservative 11;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1  UAUGAUUUUUUUUUAAGCCCUAGGGGC 28
       :|:::|:::|:::|:::|:::|
Db      19  TATGATCTTTTGTAGCCCTAGGGGC 46

RESULT 9
BD274268
LOCUS      Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION  BD274268
VERSION    BD274268.1  GI:33084036
KEYWORDS   JP 2002526030-A/235.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
            1 (bases 1 to 46)
REFERENCE  Ecker,D.J., Sampath,R., Griffee,R. and Mcneil,J.
AUTHORS    Identification of molecular interaction sites in RNA for novel drug
TITLE      discovery
JOURNAL    Patent: JP 2002526030-A 235 20-AUG-2002;
ISIS       PHARMACEUTICALS INC
OS         Artificial Sequence
PN         JP 2002526030-A/235
PD         20-AUG-2002
PR         12-MAY-1999 JP 20000548510
PR         12-MAY-1998 US 60/085092,12-MAY-1998 US
          09/076440 PI

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DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
FT /organism='Artificial Sequence'.
Location/Qualifiers

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source
1..46

ORIGIN
/organism="synthetic construct"
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/db_xref="taxon:32630"

Query Match 96.6%; Score 28; DB 6; Length 46;

Best Local Similarity 60.7%; Pred. No. 0.061;
Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCUAGGGGC 28

Db 19 TATGATCTTTTGTAGCCCTAGGGGC 46

RESULT 10

BD274269

LOCUS BD274269 46 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.

ACCESSION BD274269

VERSION BD274269.1 GI:33084037

KEYWORDS JP 2002526030-A/236.

SOURCE synthetic construct

ORGANISM artificial construct

artificial sequences.

1 (bases 1 to 46)

REFERENCE Ecker, D.J., Sampath, R., Griffey, R. and Mcneil, J.

AUTHORS Identification of molecular interaction sites in RNA for novel drug

TITLE discovery

JOURNAL Patent: JP 2002526030-A 236 20-AUG-2002;

COMMENT ISIS PHARMACEUTICALS INC

OS Artificial Sequence

PN JP 2002526030-A/236

PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510

PR 12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI

DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC

C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description

of Artificial Sequence: Novel Sequence FH Key

Location/Qualifiers

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FT /organism='Artificial Sequence'.
Location/Qualifiers

FEATURES source 1..46

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/db_xref="taxon:32630"

ORIGIN

Query Match 96.6%; Score 28; DB 6; Length 46;

Best Local Similarity 60.7%; Pred. No. 0.061;

Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCUAGGGGC 28

Db 19 TATGATCTTTTGTAGCCCTAGGGGC 46

RESULT 11

BD274270

LOCUS BD274270 42 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.

ACCESSION BD274270

VERSION BD274270.1 GI:33084038

KEYWORDS

SOURCE JP 2002526030-A/237.

ORGANISM synthetic construct

artificial sequences.

1 (bases 1 to 42)

REFERENCE Ecker, D.J., Sampath, R., Griffey, R. and Mcneil, J.

AUTHORS Identification of molecular interaction sites in RNA for novel drug

TITLE discovery

JOURNAL Patent: JP 2002526030-A 237 20-AUG-2002;

COMMENT ISIS PHARMACEUTICALS INC

OS Artificial Sequence

PN JP 2002526030-A/237

PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510

PR 12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI

DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC

C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description

of Artificial Sequence: Novel Sequence FH Key

Location/Qualifiers

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Location/Qualifiers

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Query Match 89.0%; Score 25.8; DB 6; Length 42;

Best Local Similarity 55.2%; Pred. No. 0.63;

Matches 16; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCUAGGGGC 29

Db 4 TAGATCTTTTGTAGCCCTAGGGCT 32

RESULT 12

BD274278

LOCUS BD274278 42 bp RNA linear PAT 17-JUL-2003

DEFINITION Identification of molecular interaction sites in RNA for novel drug

discovery.

ACCESSION BD274278

VERSION BD274278.1 GI:33084046

KEYWORDS JP 2002526030-A/245.

SOURCE synthetic construct

artificial sequences.

1 (bases 1 to 42)

REFERENCE Ecker, D.J., Sampath, R., Griffey, R. and Mcneil, J.

AUTHORS Identification of molecular interaction sites in RNA for novel drug

TITLE discovery

JOURNAL Patent: JP 2002526030-A 245 20-AUG-2002;

COMMENT ISIS PHARMACEUTICALS INC

OS Artificial Sequence

PN JP 2002526030-A/245

PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510

PR 12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI

DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC

C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description

of Artificial Sequence: Novel Sequence FH Key

Location/Qualifiers

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FT /organism='Artificial Sequence'.
Location/Qualifiers

FEATURES source 1..42

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/db_xref="taxon:32630"

ORIGIN

Query Match 89.0%; Score 25.8; DB 6; Length 42;

Best Local Similarity 55.2%; Pred. No. 0.63;
Matches 16; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCCUAGGGGC 29
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Db 4 TAAGATCTTTTGTAAAGCCCTACGGCT 32

RESULT 13
BD274238
LOCUS BD274238 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274238.1 GI:33084006
VERSION JP 2002526030-A/205.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 46)
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery

JOURNAL Patent: JP 2002526030-A 205 20-AUG-2002;

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/205
PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence PH Key

Location/Qualifiers
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FEATURES
source

ORIGIN

Query Match 85.5%; Score 24.8; DB 6; Length 46;
Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 16; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCCUAGGGGC 28
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Db 19 TAAGATCTTTTGTAAAGCCCTACGGGC 46

RESULT 14
BD274256
LOCUS BD274256 46 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274256.1 GI:33084024
VERSION JP 2002526030-A/223.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 46)
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery

JOURNAL Patent: JP 2002526030-A 223 20-AUG-2002;

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/223
PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510

PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence PH Key

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Location/Qualifiers
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/db_xref="taxon:32630"

FEATURES
source

ORIGIN

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Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 16; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCCUAGGGGC 28
: |||:||||:|||||:|||||:|||||:
Db 19 TAAGATCTTTTGTAAAGCCCTACGGGC 46

RESULT 15

BD274271
LOCUS BD274271 42 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274271.1 GI:33084039
VERSION JP 2002526030-A/238.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 42)
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery

JOURNAL Patent: JP 2002526030-A 238 20-AUG-2002;

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/238
PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510

PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence PH Key

Location/Qualifiers
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FEATURES
source

ORIGIN

Query Match 82.1%; Score 23.8; DB 6; Length 42;
Best Local Similarity 55.6%; Pred. No. 5.3;
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCCUAGGGG 27
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Db 4 TAAGATCTTTTGTAAAGCCCTACGGC 30

RESULT 16

BD274279
LOCUS BD274279 42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION


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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
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Query Match 80.0%; Score 23.2; DB 6; Length 42;
Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGUAGCCCUAGGGGCU 29
||||:||||:||||:||||:||||:
Db 5 AAGATTCCTTTTGTAAAGCCCAAGGGCT 32
||||:||||:||||:||||:||||:
RESULT 20
BD274273 42 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274273
VERSION BD274273.1 GI:33084041
KEYWORDS JP 2002526030-A/240.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 240 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/240
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGUAGCCCUAGGGGCU 29
||||:||||:||||:||||:||||:
Db 5 AAGATTCCTTTTGTAAAGCCCAAGGGCT 32
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RESULT 21
BD274280 42 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.

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ACCESSION BD274280
VERSION BD274280.1 GI:33084048
KEYWORDS JP 2002526030-A/247.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 247 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/247
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGUAGCCCUAGGGGCU 29
||||:||||:||||:||||:||||:
Db 5 AAGATTCCTTTTGTAAAGCCCAAGGGCT 32
||||:||||:||||:||||:||||:
RESULT 22
BD274281 42 bp RNA linear PAT 17-JUL-2003.
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274281
VERSION BD274281.1 GI:33084049
KEYWORDS JP 2002526030-A/248.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 248 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/248
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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ORIGIN

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Query Match      80.0%; Score 23.2; DB 6; Length 42;
Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGUAGCCCUAGGGGU 29
    |||:||||:||||:||||:||||:
Db 5 AAGATTCTTTTGTAAAGCCCAAGGGCT 32

RESULT 23
BD274284
LOCUS      42 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION  BD274284
VERSION     BD274284.1 GI:33084052
KEYWORDS   JP 2002526030-A/251.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 42)
AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE     Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL
COMMENT    Patent: JP 2002526030-A 251 20-AUG-2002;
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            OS Artificial Sequence
            PN JP 2002526030-A/251
            PD 20-AUG-2002
            PF 12-MAY-1999 JP 2000548510
            PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            Cl2Q1/68,A61K31/7105,A61K48/00,Cl2N15/09,Cl2N15/00 CC Description
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ORIGIN

Query Match      77.9%; Score 22.6; DB 6; Length 42;
Best Local Similarity 51.7%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 UAUGAUCUUUUUGUAGCCCUAGGGGU 29
    |||:||||:||||:||||:||||:
Db 4 TTTGATCCTTTCTGTAAGCCCTACGGGCT 32

RESULT 24
BD274241
LOCUS      46 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION  BD274241
VERSION     BD274241.1 GI:33084009
KEYWORDS   JP 2002526030-A/208.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE     Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL
COMMENT    Patent: JP 2002526030-A 208 20-AUG-2002;
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PD 20-AUG-2002
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PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
Cl2Q1/68,A61K31/7105,A61K48/00,Cl2N15/09,Cl2N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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/organism='Artificial Sequence'.

FEATURES
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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

ORIGIN

Query Match      76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGUAGCCCUAGGGGC 28
    |||:||||:||||:||||:||||:
Db 20 AAGATTCTTTTGTAAAGCCCAAGGGC 46

RESULT 25
BD274242
LOCUS      46 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION  BD274242
VERSION     BD274242.1 GI:33084010
KEYWORDS   JP 2002526030-A/209.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE     Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL
COMMENT    Patent: JP 2002526030-A 209 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002526030-A/209
            PD 20-AUG-2002
            PF 12-MAY-1999 JP 2000548510
            PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            Cl2Q1/68,A61K31/7105,A61K48/00,Cl2N15/09,Cl2N15/00 CC Description
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ORIGIN

Query Match      76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGUAGCCCUAGGGGC 28
    |||:||||:||||:||||:||||:
Db 20 AAGATTCTTTTGTAAAGCCCAAGGGC 46

RESULT 26
BD274243
LOCUS      46 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug

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discovery.
ACCESSION      BD274243
VERSION        BD274243.1  GI:33084011
KEYWORDS       JP 2002526030-A/210.
SOURCE         SYNTHETIC CONSTRUCT
ORGANISM       SYNTHETIC CONSTRUCT
               ARTIFICIAL SEQUENCES.
REFERENCE      1 (bases 1 to 46)
AUTHORS        Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE          Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL        Patent: JP 2002526030-A 210 20-AUG-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002526030-A/210
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
               of Artificial Sequence: Novel Sequence PH Key
Location/Qualifiers
FT source      1. .46
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1. .46
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   /db_xref="taxon:32630"

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Query Match      76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY  2 AUGAUUUUUUUUUAAGCCUAGGGGC 28
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Db   20 AAGATCTTTTGTAAAGCCCAAGGC 46

RESULT 27
BD274258
LOCUS      BD274258
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION      BD274258.1  GI:33084026
VERSION        BD274258.1  GI:33084026
KEYWORDS       JP 2002526030-A/225.
SOURCE         SYNTHETIC CONSTRUCT
ORGANISM       SYNTHETIC CONSTRUCT
               ARTIFICIAL SEQUENCES.
REFERENCE      1 (bases 1 to 46)
AUTHORS        Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE          Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL        Patent: JP 2002526030-A 225 20-AUG-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002526030-A/225
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
               of Artificial Sequence: Novel Sequence PH Key
Location/Qualifiers
FT source      1. .46
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FEATURES
source
1. .46
   /organism="synthetic construct"
   /mol_type="genomic RNA"
   /db_xref="taxon:32630"

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ORIGIN
Query Match      76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY  2 AUGAUUUUUUUUUAAGCCUAGGGGC 28
    |||:::|||||
Db   20 AAGATCTTTTGTAAAGCCCAAGGC 46

RESULT 28
BD274259
LOCUS      BD274259
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION      BD274259.1  GI:33084027
VERSION        BD274259.1  GI:33084027
KEYWORDS       JP 2002526030-A/226.
SOURCE         SYNTHETIC CONSTRUCT
ORGANISM       SYNTHETIC CONSTRUCT
               ARTIFICIAL SEQUENCES.
REFERENCE      1 (bases 1 to 46)
AUTHORS        Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE          Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL        Patent: JP 2002526030-A 226 20-AUG-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002526030-A/226
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
               of Artificial Sequence: Novel Sequence PH Key
Location/Qualifiers
FT source      1. .46
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FEATURES
source
1. .46
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   /mol_type="genomic RNA"
   /db_xref="taxon:32630"

ORIGIN
Query Match      76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY  2 AUGAUUUUUUUUUAAGCCUAGGGGC 28
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Db   20 AAGATCTTTTGTAAAGCCCAAGGC 46

RESULT 29
BD274260
LOCUS      BD274260
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION      BD274260.1  GI:33084028
VERSION        BD274260.1  GI:33084028
KEYWORDS       JP 2002526030-A/227.
SOURCE         SYNTHETIC CONSTRUCT
ORGANISM       SYNTHETIC CONSTRUCT
               ARTIFICIAL SEQUENCES.
REFERENCE      1 (bases 1 to 46)
AUTHORS        Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE          Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL        Patent: JP 2002526030-A 227 20-AUG-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence

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PN JP 2002526030-A/227
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
/organism='Artificial Sequence'.
FEATURES
source
1..46
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AUGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|
Db 20 AAGATTCTTTTGTGAAGCCCTACGGGC 46

RESULT 30
BD274246 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274246
VERSION BD274246.1 GI:33084014
KEYWORDS JP 2002526030-A/213.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 213 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/213
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
/organism='Artificial Sequence'.
FEATURES
source
1..46
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 74.5%; Score 21.6; DB 6; Length 46;
Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|
Db 19 TTGTATCCTTTCTGTGAAGCCCTACGGGC 46

RESULT 31
BD274248 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274248
VERSION BD274248.1 GI:33084016
KEYWORDS JP 2002526030-A/215.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 215 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/215
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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1..46
/organism="synthetic construct"
/mol_type="genomic RNA"
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Query Match 74.5%; Score 21.6; DB 6; Length 46;
Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
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Db 19 TTGTATCCTTTCTGTGAAGCCCTACGGGC 46

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DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274248
VERSION BD274248.1 GI:33084016
KEYWORDS JP 2002526030-A/215.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 215 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/215
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 74.5%; Score 21.6; DB 6; Length 46;
Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
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Db 19 TTGTATCCTTTCTGTGAAGCCCTACGGGC 46

RESULT 32
BD274262 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274262
VERSION BD274262.1 GI:33084030
KEYWORDS JP 2002526030-A/229.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 229 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/229
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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/organism='Artificial Sequence'.
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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 74.5%; Score 21.6; DB 6; Length 46;
Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|
Db 19 TTGTATCCTTTCTGTGAAGCCCTACGGGC 46

RESULT 33
BD274262 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274262
VERSION BD274262.1 GI:33084030
KEYWORDS JP 2002526030-A/229.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 229 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/229
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
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1..46
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ORIGIN
Query Match 74.5%; Score 21.6; DB 6; Length 46;
Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|
Db 19 TTGTATCCTTTCTGTGAAGCCCTACGGGC 46

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DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274251
VERSION BD274251.1 GI:33084019
KEYWORDS JP 2002526030-A/218.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 218 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/218
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/68,A6IK31/7105,A6IK48/00,CI2N15/09,CI2N15/00 CC Description
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FH Key Location/Qualifiers
FT misc feature (40)..(46).

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Query Match 66.9%; Score 19.4; DB 6; Length 46;
Best Local Similarity 52.4%; Pred. No. 5.6e+02;
Matches 11; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGAUUCUUUUUGUAGGCC 21
Db 19 TAAGATTCTTTTGTAGGCC 39

RESULT 37
LOCUS BD274255
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274255
VERSION BD274255.1 GI:33084023
KEYWORDS JP 2002526030-A/222.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 222 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/222
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/68,A6IK31/7105,A6IK48/00,CI2N15/09,CI2N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc feature (40)..(46).

FEATURES
source
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

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Query Match 66.9%; Score 19.4; DB 6; Length 46;
Best Local Similarity 52.4%; Pred. No. 5.6e+02;
Matches 11; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGAUUCUUUUUGUAGGCC 21
Db 19 TAAGATTCTTTTGTAGGCC 39

RESULT 38
LOCUS BD274267
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274267
VERSION BD274267.1 GI:33084035
KEYWORDS JP 2002526030-A/234.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 234 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/234
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/68,A6IK31/7105,A6IK48/00,CI2N15/09,CI2N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc feature (40)..(46).

FEATURES
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/organism="synthetic construct"
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ORIGIN

Query Match 66.9%; Score 19.4; DB 6; Length 46;
Best Local Similarity 52.4%; Pred. No. 5.6e+02;
Matches 11; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGAUUCUUUUUGUAGGCC 21
Db 19 TAAGATTCTTTTGTAGGCC 39

RESULT 39
LOCUS BD274274
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274274
VERSION BD274274.1 GI:33084042
KEYWORDS JP 2002526030-A/241.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 241 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/241
PD 20-AUG-2002

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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
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Location/Qualifiers
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FEATURES
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ORIGIN

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Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
QY 10 UUUGUAGGCCCUAGGGGU 29
Db 13 TTTTGTAGCCCTAGGGCT 32

RESULT 40

BD274282
LOCUS 42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274282
VERSION BD274282.1 GI:33084050
KEYWORDS JP 2002526030-A/249.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 249 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/249
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1. .42
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Location/Qualifiers
1. .42
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/mol_type='genomic RNA'
/db_xref='taxon:32630'

FEATURES
source

ORIGIN

Query Match 63.4%; Score 18.4; DB 6; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
QY 10 UUUGUAGGCCCUAGGGGU 29
Db 13 TTTTGTAGCCCTAGGGCT 32

Search completed: April 18, 2004, 08:41:23
Job time : 765.333 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:09:18 ; Search time 746.333 Seconds
(without alignments)
1684.164 Million cell updates/sec

Title: US-09-310-844C-23
Perfect score: 29
Sequence: 1 nngauncuuunnguaagccnangnngn 29

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1774092

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.on.*
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- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
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- 12: gb.sy.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	62.1	42	6	BD274271	BD274271 Identific
3	18	62.1	42	6	BD274272	BD274272 Identific
4	18	62.1	42	6	BD274273	BD274273 Identific
5	18	62.1	42	6	BD274275	BD274275 Identific
6	18	62.1	42	6	BD274278	BD274278 Identific
7	18	62.1	42	6	BD274279	BD274279 Identific
8	18	62.1	42	6	BD274280	BD274280 Identific
9	18	62.1	42	6	BD274281	BD274281 Identific
10	18	62.1	42	6	BD274283	BD274283 Identific
11	18	62.1	42	6	BD274284	BD274284 Identific
12	18	62.1	44	6	BD274277	BD274277 Identific
13	18	62.1	46	6	BD274238	BD274238 Identific
14	18	62.1	46	6	BD274240	BD274240 Identific
15	18	62.1	46	6	BD274241	BD274241 Identific
16	18	62.1	46	6	BD274242	BD274242 Identific
17	18	62.1	46	6	BD274243	BD274243 Identific
18	18	62.1	46	6	BD274246	BD274246 Identific
19	18	62.1	46	6	BD274247	BD274247 Identific
20	18	62.1	46	6	BD274248	BD274248 Identific
21	18	62.1	46	6	BD274249	BD274249 Identific
22	18	62.1	46	6	BD274252	BD274252 Identific
23	18	62.1	46	6	BD274253	BD274253 Identific
24	18	62.1	46	6	BD274256	BD274256 Identific
25	18	62.1	46	6	BD274257	BD274257 Identific
26	18	62.1	46	6	BD274258	BD274258 Identific
27	18	62.1	46	6	BD274259	BD274259 Identific
28	18	62.1	46	6	BD274260	BD274260 Identific
29	18	62.1	46	6	BD274262	BD274262 Identific
30	18	62.1	46	6	BD274263	BD274263 Identific
31	18	62.1	46	6	BD274264	BD274264 Identific
32	18	62.1	46	6	BD274265	BD274265 Identific
33	18	62.1	46	6	BD274268	BD274268 Identific
34	18	62.1	46	6	BD274269	BD274269 Identific
35	15	51.7	46	6	BD274237	BD274237 Identific
36	15	51.7	46	6	BD274251	BD274251 Identific
37	15	51.7	46	6	BD274255	BD274255 Identific
38	15	51.7	46	6	BD274267	BD274267 Identific
39	14.8	51.0	42	6	BD274276	BD274276 Identific
40	13	44.8	42	6	BD274274	BD274274 Identific
41	13	44.8	42	6	BD274282	BD274282 Identific
C 42	12.8	44.1	53	10	MDTRVNB	X63580 M.domesticu
43	12.8	44.1	57	8	AJ591789	AJ591789 Arabidops
44	12.8	44.1	68	6	AR356644	AR356644 Sequence
45	12.2	42.1	27	6	AR364272	AR364272 Sequence
C 46	12.2	42.1	30	6	AX792238	AX792238 Sequence
47	12.2	42.1	44	6	AX008706	AX008706 Sequence
C 48	12.2	42.1	45	6	AX008707	AX008707 Sequence
49	12.2	42.1	69	6	AR052906	AR052906 Sequence
50	12.2	42.1	69	6	AR054269	AR054269 Sequence
51	12.2	42.1	69	6	AR054471	AR054471 Sequence
C 52	12.2	42.1	70	6	A42881	A42881 Sequence 13
53	12.2	42.1	70	6	AR271415	AR271415 Sequence
C 54	12.2	42.1	73	6	E02131	E02131 Pseudoknot
C 55	12	41.4	24	6	AX291705	AX291705 Sequence
56	11.8	40.7	21	6	AR080204	AR080204 Sequence
57	11.8	40.7	21	6	AX088729	AX088729 Sequence
C 58	11.8	40.7	21	6	AX088730	AX088730 Sequence
59	11.8	40.7	21	6	BD023126	BD023126 Glutathio
C 60	11.8	40.7	33	10	MDTRVNB	X63589 M.domesticu
C 61	11.8	40.7	40	10	MDTRVNB	X63579 M.domesticu
C 62	11.8	40.7	46	10	MDTRVNB	X63581 M.domesticu
63	11.8	40.7	47	6	A82690	A82690 Sequence 35
64	11.8	40.7	47	6	A82705	A82705 Sequence 50
C 65	11.8	40.7	51	10	MDTRVNB	X63582 M.domesticu

66	11.8	40.7	65	6	AX483016	Sequence	139	11.2	38.6	60	6	I02058	Sequence 2
67	11.8	40.7	68	7	PTCLSL	M1570 Bacteriophage	140	11.2	38.6	65	6	AX484904	Sequence
68	11.8	40.7	76	10	MUSGLU	M26768 Mus musculus	141	11.2	38.6	70	6	AX123764	Sequence
69	11.8	40.7	77	6	AX092950	Sequence	142	11.2	38.6	75	7	PTSPJ5	M11608 Bacteriophage
70	11.8	40.7	77	6	AX092951	Sequence	C 143	11.2	38.6	75	11	AGRPD33T7	268578 A.gambiae S
71	11.8	40.7	77	6	AX167320	Sequence	C 144	11.2	38.6	78	6	AX775388	Sequence
72	11.8	40.7	77	6	AX167321	Sequence	C 145	11.2	38.6	78	6	AX729713	Sequence
73	11.6	40.0	24	6	AX721991	Sequence	146	11	37.9	17	6	AX730441	Sequence
74	11.6	40.0	31	6	AX425989	Sequence	147	11	37.9	17	6	AX757729	Sequence
75	11.6	40.0	36	6	AX176463	Sequence	C 148	11	37.9	25	6	AX772858	Sequence
76	11.6	40.0	36	6	AX176468	Sequence	C 149	11	37.9	29	6	E30622	E30622 Antibody an
77	11.6	40.0	56	6	AX247478	Sequence	C 150	11	37.9	29	6	E30622	E30622 Antibody an
78	11.6	40.0	57	9	S78643	S78643 Ig VH3A10-I	151	11	37.9	30	6	E31231	E31231 Device for
79	11.6	40.0	60	12	SYNNAVAA	M60029 Avian neovi	C 152	11	37.9	30	6	AX790824	Sequence
80	11.6	40.0	60	12	SYNNAVAP	M60085 Avian neovi	C 153	11	37.9	31	6	AR002540	Sequence
81	11.6	40.0	61	6	AX233863	Sequence	C 154	11	37.9	31	6	AR111585	Sequence
82	11.6	40.0	70	6	BD107373	BD107373 DNA conta	C 155	11	37.9	31	6	AR148499	Sequence
83	11.4	39.3	17	6	AX72857	Sequence	C 156	11	37.9	31	6	AR158211	Sequence
84	11.4	39.3	17	6	AX728660	Sequence	C 157	11	37.9	31	6	I93721	I93721 Sequence 71
85	11.4	39.3	32	17	HSMC42B09	X88068 H.sapiens D	C 158	11	37.9	31	6	AR267786	Sequence
86	11.4	39.3	36	6	A61637	A61637 Sequence 32	C 159	11	37.9	31	6	AR365821	Sequence
87	11.4	39.3	40	6	AX306333	Sequence	C 160	11	37.9	32	6	BD174747	BD174747 Method fo
88	11.4	39.3	44	6	BD274261	Sequence	161	11	37.9	33	6	E15490	E15490 Primer. 7/1
89	11.4	39.3	44	8	AJ596054	AJ596054 Arabidops	162	11	37.9	34	6	AR381466	Sequence
90	11.4	39.3	46	6	BD274245	BD274245 Identific	163	11	37.9	34	6	AR381469	Sequence
91	11.4	39.3	49	6	AX555177	Sequence	C 164	11	37.9	54	6	AX297550	Sequence
92	11.4	39.3	51	6	AR204359	Sequence	C 165	11	37.9	69	5	AF259080	AF259080 Agkistrod
93	11.4	39.3	65	6	AR405872	Sequence	C 166	11	37.9	69	5	AF259081	AF259081 Agkistrod
94	11.4	39.3	65	6	BD190619	BD190619 Bioreacti	167	11	37.9	70	6	AR054896	Sequence
95	11.4	39.3	70	4	BOVMTTRV	K00258 Bovine mito	168	11	37.9	70	6	AR066161	Sequence
96	11.2	38.6	20	6	AX293832	Sequence	169	10.8	37.2	17	6	AR673540	Sequence
97	11.2	38.6	24	6	AX288322	Sequence	C 170	10.8	37.2	17	6	AX727506	Sequence
98	11.2	38.6	24	6	AX289199	Sequence	C 171	10.8	37.2	17	6	AX730387	Sequence
99	11.2	38.6	24	6	AX801575	Sequence	C 172	10.8	37.2	17	6	AX733947	Sequence
100	11.2	38.6	24	6	AX801575	Sequence	C 173	10.8	37.2	17	6	AX736200	Sequence
101	11.2	38.6	25	6	AR020995	Sequence	C 174	10.8	37.2	17	6	AX736846	Sequence
102	11.2	38.6	25	6	AR043410	Sequence	C 175	10.8	37.2	17	6	AX762433	Sequence
103	11.2	38.6	25	6	AR062325	Sequence	C 176	10.8	37.2	17	6	AX762433	Sequence
104	11.2	38.6	25	6	AR183784	Sequence	C 177	10.8	37.2	19	6	E08916	E08916 Synthetic n
105	11.2	38.6	25	6	AR368167	Sequence	C 178	10.8	37.2	19	6	E08918	E08918 Synthetic n
106	11.2	38.6	30	6	AX793341	Sequence	C 179	10.8	37.2	19	6	E09340	E09340 Oligonucleo
107	11.2	38.6	32	6	AX085951	Sequence	C 180	10.8	37.2	19	6	E09342	E09342 Oligonucleo
108	11.2	38.6	33	6	AR020996	Sequence	C 181	10.8	37.2	19	6	E09645	E09645 Oligonucleo
109	11.2	38.6	33	6	AR043411	Sequence	C 182	10.8	37.2	19	6	E11791	E11791 DNA sequenc
110	11.2	38.6	33	6	AR062326	Sequence	C 183	10.8	37.2	19	6	E11793	E11793 DNA sequenc
111	11.2	38.6	33	6	AR183785	Sequence	C 184	10.8	37.2	19	6	I49659	I49659 Sequence 1
112	11.2	38.6	34	6	BD061930	BD061930 Antigenic	C 185	10.8	37.2	19	6	I49661	I49661 Sequence 3
113	11.2	38.6	34	6	BD061930	Sequence	C 186	10.8	37.2	20	6	AR157136	AR157136 Sequence
114	11.2	38.6	36	6	E49126	E49126 Novel G pro	C 187	10.8	37.2	20	6	AX056605	AX056605 Sequence
115	11.2	38.6	40	6	E50836	E50836 Novel G pro	C 188	10.8	37.2	22	4	DOGPI601	LI5650 Dog (Clone:
116	11.2	38.6	40	6	AX516743	Sequence	C 189	10.8	37.2	22	6	AX551658	AX551658 Sequence
117	11.2	38.6	41	6	AR253879	Sequence	C 190	10.8	37.2	22	6	AX551661	AX551661 Sequence
118	11.2	38.6	41	6	AR253879	Sequence	C 191	10.8	37.2	22	6	AX551664	AX551664 Sequence
119	11.2	38.6	41	6	AR410230	Sequence	C 192	10.8	37.2	22	6	AX703148	AX703148 Sequence
120	11.2	38.6	41	6	AX316543	Sequence	C 193	10.8	37.2	22	6	AX703151	AX703151 Sequence
121	11.2	38.6	41	6	AX516847	Sequence	C 194	10.8	37.2	22	6	AX703154	AX703154 Sequence
122	11.2	38.6	41	6	AX516946	Sequence	C 195	10.8	37.2	25	6	AR434674	AR434674 Sequence
123	11.2	38.6	41	6	AX519357	Sequence	C 196	10.8	37.2	25	6	AR434675	AR434675 Sequence
124	11.2	38.6	41	6	AX519457	Sequence	C 197	10.8	37.2	25	6	AR434676	AR434676 Sequence
125	11.2	38.6	41	12	SYNNAVAY	M60106 Avian neovi	C 198	10.8	37.2	25	6	AR434677	AR434677 Sequence
126	11.2	38.6	47	6	AR291107	AR291107 Sequence	C 199	10.8	37.2	25	6	AR434678	AR434678 Sequence
127	11.2	38.6	47	6	AX194690	AX194690 Sequence	C 200	10.8	37.2	25	6	AR434679	AR434679 Sequence
128	11.2	38.6	51	10	MUSTCBBYBF	M36458 Mouse T-cel	C 201	10.8	37.2	25	6	AR434680	AR434680 Sequence
129	11.2	38.6	52	6	BD270556	BD270556 Family of	C 202	10.8	37.2	25	6	AR434681	AR434681 Sequence
130	11.2	38.6	52	6	AR208953	Sequence	C 203	10.8	37.2	25	6	AX117400	AX117400 Sequence
131	11.2	38.6	52	6	AR228346	Sequence	C 204	10.8	37.2	25	6	BD061691	BD061691 Antigenic
132	11.2	38.6	52	6	AX046943	Sequence	C 205	10.8	37.2	27	6	AR143875	AR143875 Sequence
133	11.2	38.6	52	6	AX428345	Sequence	C 206	10.8	37.2	27	6	AR161612	AR161612 Sequence
134	11.2	38.6	52	6	BD082716	BD082716 Family of	C 207	10.8	37.2	29	6	BD250919	BD250919 A plant d
135	11.2	38.6	52	12	SYNNAVAS	M60097 Avian neovi	C 208	10.8	37.2	33	6	BD107554	BD107554 Nucleic a
136	11.2	38.6	55	3	S55610S2	S55612 Broad-Compl	C 209	10.8	37.2	35	6	AX020425	AX020425 Sequence
137	11.2	38.6	59	10	CRUDELNIF	M27128 Chinese Ham	C 210	10.8	37.2	35	11	C75832	C75832 Homo sapien
138	11.2	38.6	60	6	AL5400	AL5400 Synthetic P	C 211	10.8	37.2	40	6	BD273100	BD273100 Oral immu

C 212	10.8	37.2	40	6	BD107566	BD107566 Nucleic a	C 285	10.6	36.6	36	6	A47633	A47633 Sequence 10
C 213	10.8	37.2	41	6	AX516773	AX516773 Sequence	C 286	10.6	36.6	36	6	I82277	I82277 Sequence 10
C 214	10.8	37.2	42	6	AX513792	AX513792 Sequence	C 287	10.6	36.6	38	6	AX307598	AX307598 Sequence
C 215	10.8	37.2	42	9	HSDU26980	U26980 Human isola	C 288	10.6	36.6	38	6	BD003217	BD003217 Method fo
C 216	10.8	37.2	43	6	AX484567	AX484567 Sequence	C 289	10.6	36.6	41	6	AX514720	AX514720 Sequence
C 217	10.8	37.2	43	6	AX033518	AX033518 Sequence	C 290	10.6	36.6	41	6	AX520728	AX520728 Sequence
C 218	10.8	37.2	45	6	AX033518	AX033518 Sequence	C 291	10.6	36.6	43	6	BD142503	BD142503 A method
C 219	10.8	37.2	45	6	I29258	I29258 Sequence 13	C 292	10.6	36.6	43	6	BD142503	BD142503 A method
C 220	10.8	37.2	45	6	I29470	I29470 Sequence 13	C 293	10.6	36.6	43	6	BD142503	BD142503 A method
C 221	10.8	37.2	45	6	I30932	I30932 Sequence 34	C 294	10.6	36.6	44	5	ATH553793	ATH553793 Arabidops
C 222	10.8	37.2	45	6	I91144	I91144 Sequence 34	C 295	10.6	36.6	47	6	AR290538	AR290538 Sequence
C 223	10.8	37.2	45	6	AR209182	AR209182 Sequence	C 296	10.6	36.6	48	13	S76577	S76577 TCR alpha =
C 224	10.8	37.2	45	6	AR209394	AR209394 Sequence	C 297	10.6	36.6	50	6	AR164552	AR164552 Sequence
C 225	10.8	37.2	45	6	AR290551	AR290551 Sequence	C 298	10.6	36.6	54	6	A57940	A57940 Sequence 6
C 226	10.8	37.2	47	6	AR291810	AR291810 Sequence	C 299	10.6	36.6	55	8	AJ588102	AJ588102 Arabidops
C 227	10.8	37.2	48	6	I15164	I15164 Sequence 13	C 300	10.6	36.6	60	6	A38757	A38757 Sequence 7
C 228	10.8	37.2	50	6	A21306	A21306 Nucleotide	C 301	10.6	36.6	60	6	I89875	I89875 Sequence 7
C 229	10.8	37.2	50	6	AR033731	AR033731 Sequence	C 302	10.6	36.6	60	10	MUSHPRT5	MUSHPRT5
C 230	10.8	37.2	50	6	AR064653	AR064653 Sequence	C 303	10.6	36.6	63	6	AX384573	AX384573 Sequence
C 231	10.8	37.2	50	6	BD273138	BD273138 Oral immu	C 304	10.6	36.6	64	6	AX270680	AX270680 Sequence
C 232	10.8	37.2	50	6	I29471	I29471 Sequence 34	C 305	10.6	36.6	64	6	AX272211	AX272211 Sequence
C 233	10.8	37.2	50	6	I91145	I91145 Sequence 34	C 306	10.6	36.6	65	6	AX485715	AX485715 Sequence
C 234	10.8	37.2	50	6	AR209395	AR209395 Sequence	C 307	10.6	36.6	65	6	AX486452	AX486452 Sequence
C 235	10.8	37.2	51	6	AR090925	AR090925 Sequence	C 308	10.6	36.6	66	1	ECOLETXX	ECOLETXX
C 236	10.8	37.2	51	6	AR053680	AR053680 Sequence	C 309	10.6	36.6	68	5	AF125363	AF125363 Polyodon
C 237	10.8	37.2	51	6	AR060991	AR060991 Sequence	C 310	10.6	36.6	69	6	AR171551	AR171551 Sequence
C 238	10.8	37.2	51	6	AR087722	AR087722 Sequence	C 311	10.6	36.6	69	6	BD005571	BD005571 Compositi
C 239	10.8	37.2	51	6	AX178113	AX178113 Sequence	C 312	10.6	36.6	70	6	AX315526	AX315526 Sequence
C 240	10.8	37.2	51	6	I74699	I74699 Sequence 39	C 313	10.6	36.6	70	6	BD051059	BD051059 Sequence
C 241	10.8	37.2	51	6	AR287993	AR287993 Sequence	C 314	10.6	36.6	71	10	MMU403504	MMU403504 M.musculu
C 242	10.8	37.2	51	6	AX360127	AX360127 Sequence	C 315	10.6	36.6	72	1	ECOPKYD2	ECOPKYD2
C 243	10.8	37.2	51	6	AX117401	AX117401 Sequence	C 316	10.6	36.6	73	8	AY203293	AY203293 Arabidops
C 244	10.8	37.2	51	6	AX118033	AX118033 Sequence	C 317	10.6	36.6	78	9	AY256011	AY256011 Macaca mu
C 245	10.8	37.2	51	6	AX190386	AX190386 Sequence	C 318	10.4	35.9	17	6	AX217417	AX217417 Sequence
C 246	10.8	37.2	53	10	MUSCXBVB	M36462 Mouse T-cel	C 319	10.4	35.9	17	6	AX217784	AX217784 Sequence
C 247	10.8	37.2	58	10	MUSCXBVBH	M36460 Mouse T-cel	C 320	10.4	35.9	17	6	AX218162	AX218162 Sequence
C 248	10.8	37.2	58	10	MUSCXBVB	M36459 Mouse T-cel	C 321	10.4	35.9	17	6	AX304795	AX304795 Sequence
C 249	10.8	37.2	59	10	MUSCXBVB	M36463 Mouse T-cel	C 322	10.4	35.9	20	6	AR293822	AR293822 Sequence
C 250	10.8	37.2	61	6	AR355618	AR355618 Sequence	C 323	10.4	35.9	20	6	AR350263	AR350263 Sequence
C 251	10.8	37.2	62	10	MUSCXBVB	M36457 Mouse T-cel	C 324	10.4	35.9	21	6	AX096878	AX096878 Sequence
C 252	10.8	37.2	65	6	AX483200	AX483200 Sequence	C 325	10.4	35.9	24	6	AX445741	AX445741 Sequence
C 253	10.8	37.2	65	6	AX485901	AX485901 Sequence	C 326	10.4	35.9	25	8	ATH526250	ATH526250 Arabidops
C 254	10.8	37.2	65	6	AX486309	AX486309 Sequence	C 327	10.4	35.9	25	8	ATH526284	ATH526284 Arabidops
C 255	10.8	37.2	68	8	ATH521374	ATH521374 Arabidops	C 328	10.4	35.9	27	6	BD001453	BD001453 Sequence
C 256	10.8	37.2	72	11	AL806183	AL806183 Arabidops	C 329	10.4	35.9	27	6	BD000823	BD000823 Amplifica
C 257	10.8	37.2	77	8	AJ593524	AJ593524 Arabidops	C 330	10.4	35.9	27	6	BD166181	BD166181 Amplifica
C 258	10.6	36.6	23	6	E09974	E09974 Primer for	C 331	10.4	35.9	28	8	ATH522549	ATH522549 Arabidops
C 259	10.6	36.6	23	6	E30118	E30118 PCR primer	C 332	10.4	35.9	29	6	AR096942	AR096942 Sequence
C 260	10.6	36.6	24	6	E58779	E58779 Novel human	C 333	10.4	35.9	29	6	BD136137	BD136137 Vaccines
C 261	10.6	36.6	24	6	AX768391	AX768391 Sequence	C 334	10.4	35.9	30	6	AX155197	AX155197 Sequence
C 262	10.6	36.6	28	6	AX027376	AX027376 Sequence	C 335	10.4	35.9	30	6	BD061572	BD061572 D-aminoac
C 263	10.6	36.6	28	6	E05018	E05018 Primer. 9/1	C 336	10.4	35.9	30	9	HUMPLTP09	HUMPLTP09
C 264	10.6	36.6	30	6	AR079815	AR079815 Sequence	C 337	10.4	35.9	31	6	BD002393	BD002393 Gene comp
C 265	10.6	36.6	30	6	AR182366	AR182366 Sequence	C 338	10.4	35.9	31	6	BD002854	BD002854 Gene comp
C 266	10.6	36.6	30	6	AX321657	AX321657 Sequence	C 339	10.4	35.9	36	6	AX14290	AX14290 oligonucleo
C 267	10.6	36.6	30	6	AX793354	AX793354 Sequence	C 340	10.4	35.9	36	6	A14291	A14291 oligonucleo
C 268	10.6	36.6	30	6	BD014351	BD014351 Plant pro	C 341	10.4	35.9	36	6	AX770369	AX770369 Sequence
C 269	10.6	36.6	31	6	AX274078	AX274078 Sequence	C 342	10.4	35.9	36	6	AX805507	AX805507 Sequence
C 270	10.6	36.6	31	6	AX274083	AX274083 Sequence	C 343	10.4	35.9	36	6	AX805508	AX805508 Sequence
C 271	10.6	36.6	31	6	AX274267	AX274267 Sequence	C 344	10.4	35.9	36	6	AX805509	AX805509 Sequence
C 272	10.6	36.6	31	6	AX425824	AX425824 Sequence	C 345	10.4	35.9	39	6	AX576868	AX576868 Sequence
C 273	10.6	36.6	31	6	AX425978	AX425978 Sequence	C 346	10.4	35.9	39	6	AX576868	AX576868 Sequence
C 274	10.6	36.6	31	6	AX426018	AX426018 Sequence	C 347	10.4	35.9	40	6	AR211425	AR211425 Sequence
C 275	10.6	36.6	31	6	AX426065	AX426065 Sequence	C 348	10.4	35.9	40	6	AX001534	AX001534 Sequence
C 276	10.6	36.6	31	6	AX582413	AX582413 Sequence	C 349	10.4	35.9	40	6	AX001546	AX001546 Sequence
C 277	10.6	36.6	31	6	AX582509	AX582509 Sequence	C 350	10.4	35.9	41	6	AR083451	AR083451 Sequence
C 278	10.6	36.6	31	6	AX582707	AX582707 Sequence	C 351	10.4	35.9	41	6	AX515077	AX515077 Sequence
C 279	10.6	36.6	31	6	AX582713	AX582713 Sequence	C 352	10.4	35.9	41	6	AX517004	AX517004 Sequence
C 280	10.6	36.6	31	6	AX582742	AX582742 Sequence	C 353	10.4	35.9	41	6	AX518661	AX518661 Sequence
C 281	10.6	36.6	34	6	AX774183	AX774183 Sequence	C 354	10.4	35.9	41	6	AX518935	AX518935 Sequence
C 282	10.6	36.6	34	6	AX923320	AX923320 Sequence	C 355	10.4	35.9	41	6	AX518936	AX518936 Sequence
C 283	10.6	36.6	35	6	A47631	A47631 Sequence 8	C 356	10.4	35.9	41	6	AX519515	AX519515 Sequence
C 284	10.6	36.6	35	6	I82275	I82275 Sequence 8	C 357	10.4	35.9	41	6	AX521064	AX521064 Sequence

C 358	10.4	35.9	43	6	AX483586	AX483586 Sequence	C 431	10.2	35.2	24	6	BD141353	BD141353 Novel phi
C 359	10.4	35.9	45	10	MMTCRA235	X70719 M. musculus	C 432	10.2	35.2	24	6	BD142847	BD142847 Novel G P
C 360	10.4	35.9	47	6	AR288398	AR288398 Sequence	C 433	10.2	35.2	24	6	BD170822	BD170822 Process I
C 361	10.4	35.9	47	6	AR288695	AR288695 Sequence	C 434	10.2	35.2	24	6	BD181657	BD181657 Novel phi
C 362	10.4	35.9	47	6	AR288999	AR288999 Sequence	C 435	10.2	35.2	25	6	BD245582	BD245582 Developme
C 363	10.4	35.9	47	6	AR291157	AR291157 Sequence	C 436	10.2	35.2	25	6	AX472516	AX472516 Sequence
C 364	10.4	35.9	47	6	AR291884	AR291884 Sequence	C 437	10.2	35.2	26	6	BD177543	BD177543 Method fo
C 365	10.4	35.9	47	6	AX378367	AX378367 Sequence	C 438	10.2	35.2	29	6	AX394123	AX394123 Sequence
C 366	10.4	35.9	50	6	AR437951	AR437951 Sequence	C 439	10.2	35.2	30	6	AS6993	AS6993 Sequence 51
C 367	10.4	35.9	50	6	AX303593	AX303593 Sequence	C 440	10.2	35.2	30	6	AR054072	AR054072 Sequence
C 368	10.4	35.9	50	6	AX910776	AX910776 Sequence	C 441	10.2	35.2	30	6	AR127461	AR127461 Sequence
C 369	10.4	35.9	51	6	BD046309	BD046309 Sequence	C 442	10.2	35.2	30	6	I39960	I39960 Sequence 13
C 370	10.4	35.9	51	6	AX158923	AX158923 Sequence	C 443	10.2	35.2	30	6	AX474312	AX474312 Sequence
C 371	10.4	35.9	51	6	AX158924	AX158924 Sequence	C 444	10.2	35.2	31	6	AR072430	AR072430 Sequence
C 372	10.4	35.9	51	6	AX162574	AX162574 Sequence	C 445	10.2	35.2	31	6	I26541	I26541 Sequence 23
C 373	10.4	35.9	55	6	AR426960	AR426960 Sequence	C 446	10.2	35.2	33	6	AR194376	AR194376 Sequence
C 374	10.4	35.9	55	6	BD122513	BD122513 EST and e	C 447	10.2	35.2	33	6	AX060364	AX060364 Sequence
C 375	10.4	35.9	57	6	AR437963	AR437963 Sequence	C 448	10.2	35.2	33	6	AX069219	AX069219 Sequence
C 376	10.4	35.9	57	6	AX303606	AX303606 Sequence	C 449	10.2	35.2	33	6	AX069219	AX069219 Sequence
C 377	10.4	35.9	59	6	AX684263	AX684263 Sequence	C 450	10.2	35.2	33	6	AX329399	AX329399 Sequence
C 378	10.4	35.9	59	6	AX905506	AX905506 Sequence	C 451	10.2	35.2	34	9	AF505532	AF505532 Homo sapi
C 379	10.4	35.9	59	6	BD041039	BD041039 Sequence	C 452	10.2	35.2	35	6	I81895	I81895 Sequence 4
C 380	10.4	35.9	60	6	AR437964	AR437964 Sequence	C 453	10.2	35.2	36	6	AX464538	AX464538 Sequence
C 381	10.4	35.9	60	6	AX303607	AX303607 Sequence	C 454	10.2	35.2	38	6	AR146220	AR146220 Sequence
C 382	10.4	35.9	60	10	MMU86744	UB6744 Mus musculus	C 455	10.2	35.2	38	6	AR307789	AR307789 Sequence
C 383	10.4	35.9	61	6	AR437950	AR437950 Sequence	C 456	10.2	35.2	39	6	AX1997	AX1997 Synthetic I
C 384	10.4	35.9	61	6	AX303592	AX303592 Sequence	C 457	10.2	35.2	39	6	AX494814	AX494814 Sequence
C 385	10.4	35.9	67	6	AX920548	AX920548 Sequence	C 458	10.2	35.2	40	6	AX167345	AX167345 Sequence
C 386	10.4	35.9	67	6	BD056081	BD056081 Sequence	C 459	10.2	35.2	40	6	AX452098	AX452098 Sequence
C 387	10.4	35.9	68	5	AB096004	AB096004 Trachurus	C 460	10.2	35.2	41	6	AX514276	AX514276 Sequence
C 388	10.4	35.9	68	5	AF125364	AF125364 Acipenser	C 461	10.2	35.2	41	6	AX515172	AX515172 Sequence
C 389	10.4	35.9	68	5	AF125365	AF125365 Acipenser	C 462	10.2	35.2	41	6	AX517966	AX517966 Sequence
C 390	10.4	35.9	68	5	AF125366	AF125366 Acipenser	C 463	10.2	35.2	41	6	AX520458	AX520458 Sequence
C 391	10.4	35.9	68	5	AF125367	AF125367 Acipenser	C 464	10.2	35.2	41	6	AX521154	AX521154 Sequence
C 392	10.4	35.9	68	5	AF125368	AF125368 Acipenser	C 465	10.2	35.2	42	6	AR079470	AR079470 Sequence
C 393	10.4	35.9	68	5	AF125369	AF125369 Acipenser	C 466	10.2	35.2	44	6	AX804136	AX804136 Sequence
C 394	10.4	35.9	68	5	AF125370	AF125370 Scaphirhy	C 467	10.2	35.2	45	6	AR003527	AR003527 Sequence
C 395	10.4	35.9	68	5	AF125371	AF125371 Scaphirhy	C 468	10.2	35.2	45	6	AR079762	AR079762 Sequence
C 396	10.4	35.9	68	5	AF125372	AF125372 Scaphirhy	C 469	10.2	35.2	45	6	AR081292	AR081292 Sequence
C 397	10.4	35.9	70	7	PMUPBN	PMUPBN	C 470	10.2	35.2	45	6	AR170652	AR170652 Sequence
C 398	10.4	35.9	70	7	PMUPBN	PMUPBN	C 471	10.2	35.2	45	6	I55640	I55640 Sequence 4
C 399	10.4	35.9	71	6	AR058848	AR058848 Sequence	C 472	10.2	35.2	45	9	HS274591	HS274591 H. sapiens j
C 400	10.4	35.9	71	6	AR063574	AR063574 Sequence	C 473	10.2	35.2	46	6	AR160662	AR160662 Sequence
C 401	10.4	35.9	71	6	AR140964	AR140964 Sequence	C 474	10.2	35.2	46	6	BD238290	BD238290 Accelerat
C 402	10.4	35.9	73	10	F322144S30	AF322173 Mus muscu	C 475	10.2	35.2	46	6	E17006	E17006 Primer. 7/1
C 403	10.4	35.9	75	4	E01677	AY112797 Sus scrof	C 476	10.2	35.2	46	6	E17038	E17038 Primer. 7/1
C 404	10.4	35.9	77	6	E01677	AY112797 DNA sequen	C 477	10.2	35.2	46	6	E17049	E17049 Primer. 7/1
C 405	10.4	35.9	77	6	E01806	E01806 DNA encodin	C 478	10.2	35.2	47	6	AR288951	AR288951 Sequence
C 406	10.4	35.9	77	6	E01808	E01808 DNA encodin	C 479	10.2	35.2	47	6	AR289362	AR289362 Sequence
C 407	10.4	35.9	77	6	E02146	E02146 DNA encodin	C 480	10.2	35.2	47	6	AR289436	AR289436 Sequence
C 408	10.4	35.9	77	6	E02398	E02398 DNA encodin	C 481	10.2	35.2	48	6	AR032579	AR032579 Sequence
C 409	10.4	35.9	77	6	AR362673	AR362673 Sequence	C 482	10.2	35.2	48	6	I29319	I29319 Sequence 19
C 410	10.4	35.9	78	3	AY013980	AY013980 Eupriat	C 483	10.2	35.2	48	6	AR209243	AR209243 Sequence
C 411	10.4	35.9	78	6	AX362675	AX362675 Sequence	C 484	10.2	35.2	48	6	S81456	S81456 T cell anti
C 412	10.4	35.9	78	8	AY596509	AY596509 Arabidops	C 485	10.2	35.2	49	6	E54534	E54534 Herpesvirus
C 413	10.2	35.2	20	6	AR156531	AR156531 Sequence	C 486	10.2	35.2	50	6	AR003085	AR003085 Sequence
C 414	10.2	35.2	20	6	AR226170	AR226170 Sequence	C 487	10.2	35.2	50	6	AR003178	AR003178 Sequence
C 415	10.2	35.2	20	6	AX929295	AX929295 Sequence	C 488	10.2	35.2	50	6	AR009028	AR009028 Sequence
C 416	10.2	35.2	21	6	AR299973	AR299973 Sequence	C 489	10.2	35.2	50	6	AR011152	AR011152 Sequence
C 417	10.2	35.2	22	6	AR139340	AR139340 Sequence	C 490	10.2	35.2	50	6	AR032854	AR032854 Sequence
C 418	10.2	35.2	22	6	AX645165	AX645165 Sequence	C 491	10.2	35.2	50	6	AR052683	AR052683 Sequence
C 419	10.2	35.2	22	6	AX377060	AX377060 Sequence	C 492	10.2	35.2	50	6	AR060994	AR060994 Sequence
C 420	10.2	35.2	23	6	AX377063	AX377063 Sequence	C 493	10.2	35.2	50	6	AR087725	AR087725 Sequence
C 421	10.2	35.2	23	6	AX377066	AX377066 Sequence	C 494	10.2	35.2	50	6	AR175116	AR175116 Sequence
C 422	10.2	35.2	23	6	AX546629	AX546629 Sequence	C 495	10.2	35.2	50	6	I17790	I17790 Sequence 19
C 423	10.2	35.2	24	6	AR361510	AR361510 Sequence	C 496	10.2	35.2	50	6	I19215	I19215 Sequence 35
C 424	10.2	35.2	24	6	AX389401	AX389401 Sequence	C 497	10.2	35.2	50	6	I20056	I20056 Sequence 19
C 425	10.2	35.2	24	6	AX290262	AX290262 Sequence	C 498	10.2	35.2	50	6	I29594	I29594 Sequence 46
C 426	10.2	35.2	24	6	AX291190	AX291190 Sequence	C 499	10.2	35.2	50	6	I74702	I74702 Sequence 42
C 427	10.2	35.2	24	6	AX922534	AX922534 Sequence	C 500	10.2	35.2	50	6	I91268	I91268 Sequence 46
C 428	10.2	35.2	24	6	AX444424	AX444424 Sequence	C 501	10.2	35.2	50	6	I91268	I91268 Sequence 46
C 429	10.2	35.2	24	6	AX539017	AX539017 Sequence	C 502	10.2	35.2	50	6	AR209518	AR209518 Sequence
C 430	10.2	35.2	24	6	BD013015	BD013015 Novel G P	C 503	10.2	35.2	50	6	AR287996	AR287996 Sequence

C 504	10.2	35.2	50	6	AR360130	Sequence	AR360130	Sequence	577	10	34.5	20	6	AR032106	Sequence
C 505	10.2	35.2	50	6	AR408190	Sequence	AR408190	Sequence	C 578	10	34.5	20	6	AR037471	Sequence
C 506	10.2	35.2	50	6	AR613170	Sequence	AR613170	Sequence	C 579	10	34.5	20	6	AR037479	Sequence
C 507	10.2	35.2	51	6	AX114917	Sequence	AX114917	Sequence	580	10	34.5	20	6	AR160740	Sequence
C 508	10.2	35.2	51	6	AX116113	Sequence	AX116113	Sequence	581	10	34.5	20	6	AR207672	Sequence
C 509	10.2	35.2	51	6	AX117849	Sequence	AX117849	Sequence	C 582	10	34.5	20	6	AR256412	Sequence
C 510	10.2	35.2	51	6	AX157907	Sequence	AX157907	Sequence	583	10	34.5	20	6	AR264998	Sequence
C 511	10.2	35.2	51	6	AX190034	Sequence	AX190034	Sequence	C 584	10	34.5	20	6	AX264998	Sequence
C 512	10.2	35.2	51	6	AX190035	Sequence	AX190035	Sequence	C 585	10	34.5	20	6	AX264998	Sequence
C 513	10.2	35.2	51	6	AX194919	Sequence	AX194919	Sequence	C 586	10	34.5	20	6	BD023651	Process f
C 514	10.2	35.2	51	6	AX194921	Sequence	AX194921	Sequence	C 587	10	34.5	20	6	BD192558	Compositi
C 515	10.2	35.2	51	6	AX204336	Sequence	AX204336	Sequence	C 588	10	34.5	21	6	AX095705	Sequence
C 516	10.2	35.2	51	10	AP005585	Mus muscu	AP005585	Mus muscu	C 589	10	34.5	22	6	AR241575	Sequence
C 517	10.2	35.2	54	3	AF276298	Parameliu	AF276298	Parameliu	C 590	10	34.5	22	6	AR254531	Sequence
C 518	10.2	35.2	54	3	AF206133	Paa spino	AF206133	Paa spino	C 591	10	34.5	22	6	BD211597	Canine an
C 519	10.2	35.2	54	5	AF206160	Limnomet	AF206160	Limnomet	C 592	10	34.5	24	6	AR24321	LS14 primer
C 520	10.2	35.2	54	5	AR062118	Sequence	AR062118	Sequence	C 593	10	34.5	24	6	AR242633	Sequence
C 521	10.2	35.2	59	6	AR062118	Sequence	AR062118	Sequence	C 594	10	34.5	24	6	AX316356	Sequence
C 522	10.2	35.2	60	6	AR201489	Sequence	AR201489	Sequence	C 595	10	34.5	25	6	AX443778	Sequence
C 523	10.2	35.2	60	6	AR357260	Sequence	AR357260	Sequence	C 596	10	34.5	25	6	AX443778	Sequence
C 524	10.2	35.2	60	6	AX364686	Sequence	AX364686	Sequence	C 597	10	34.5	25	6	AX443778	Sequence
C 525	10.2	35.2	60	6	AX491352	Sequence	AX491352	Sequence	C 598	10	34.5	25	6	AX443778	Sequence
C 526	10.2	35.2	60	6	AX772359	Sequence	AX772359	Sequence	C 599	10	34.5	25	6	AX443778	Sequence
C 527	10.2	35.2	60	6	BD223061	Compositi	BD223061	Compositi	C 600	10	34.5	25	6	AX443778	Sequence
C 528	10.2	35.2	61	8	ATH532849	Sequence	ATH532849	Sequence	C 601	10	34.5	25	6	AX443778	Sequence
C 529	10.2	35.2	62	6	AX404946	Sequence	AX404946	Sequence	C 602	10	34.5	25	6	AX443778	Sequence
C 530	10.2	35.2	63	6	AX20299	Sequence	AX20299	Sequence	C 603	10	34.5	25	6	AX443778	Sequence
C 531	10.2	35.2	64	6	AX103463	Sequence	AX103463	Sequence	C 604	10	34.5	25	6	AX443778	Sequence
C 532	10.2	35.2	64	6	AX265182	Sequence	AX265182	Sequence	C 605	10	34.5	25	6	AX443778	Sequence
C 533	10.2	35.2	65	6	AX485251	Sequence	AX485251	Sequence	C 606	10	34.5	25	6	AX443778	Sequence
C 534	10.2	35.2	65	6	AX485383	Sequence	AX485383	Sequence	C 607	10	34.5	25	6	AX443778	Sequence
C 535	10.2	35.2	65	6	BD096846	Sequence	BD096846	Sequence	C 608	10	34.5	26	6	AX443778	Sequence
C 536	10.2	35.2	66	6	AR356613	Sequence	AR356613	Sequence	C 609	10	34.5	26	6	AX443778	Sequence
C 537	10.2	35.2	66	6	AX233564	Sequence	AX233564	Sequence	C 610	10	34.5	27	6	AX443778	Sequence
C 538	10.2	35.2	66	6	AX522168	Sequence	AX522168	Sequence	C 611	10	34.5	27	6	AX443778	Sequence
C 539	10.2	35.2	70	6	AR011570	Sequence	AR011570	Sequence	C 612	10	34.5	27	6	AX443778	Sequence
C 540	10.2	35.2	70	6	AR054926	Sequence	AR054926	Sequence	C 613	10	34.5	27	6	AX443778	Sequence
C 541	10.2	35.2	70	6	AR066191	Sequence	AR066191	Sequence	C 614	10	34.5	27	6	AX443778	Sequence
C 542	10.2	35.2	70	6	I18208	Sequence	I18208	Sequence	C 615	10	34.5	27	6	AX443778	Sequence
C 543	10.2	35.2	70	10	RR4240059	Rattus no	RR4240059	Rattus no	C 616	10	34.5	27	6	AX443778	Sequence
C 544	10.2	35.2	71	6	AR017707	Sequence	AR017707	Sequence	C 617	10	34.5	27	6	AX443778	Sequence
C 545	10.2	35.2	71	6	AR094884	Sequence	AR094884	Sequence	C 618	10	34.5	28	6	AX443778	Sequence
C 546	10.2	35.2	71	6	AR165543	Sequence	AR165543	Sequence	C 619	10	34.5	29	6	AX443778	Sequence
C 547	10.2	35.2	71	6	AR304745	Sequence	AR304745	Sequence	C 620	10	34.5	29	6	AX443778	Sequence
C 548	10.2	35.2	73	7	MS2RBLSA	Sequence	MS2RBLSA	Sequence	C 621	10	34.5	30	6	AX443778	Sequence
C 549	10.2	35.2	73	12	SYNGHNDJNB	Sequence	SYNGHNDJNB	Sequence	C 622	10	34.5	30	6	AX443778	Sequence
C 550	10.2	35.2	73	12	SYNGHNDJNC	Sequence	SYNGHNDJNC	Sequence	C 623	10	34.5	30	6	AX443778	Sequence
C 551	10.2	35.2	74	6	AX187568	Sequence	AX187568	Sequence	C 624	10	34.5	30	6	AX443778	Sequence
C 552	10.2	35.2	75	3	AF489510	Asterias	AF489510	Asterias	C 625	10	34.5	31	6	AX443778	Sequence
C 553	10.2	35.2	75	3	AF312283	Sequence	AF312283	Sequence	C 626	10	34.5	31	6	AX443778	Sequence
C 554	10.2	35.2	77	3	SRH0X3A	Sequence	SRH0X3A	Sequence	C 627	10	34.5	31	6	AX443778	Sequence
C 555	10.2	35.2	77	10	MMU543401	Mus muscu	MMU543401	Mus muscu	C 628	10	34.5	31	6	AX443778	Sequence
C 556	10.2	35.2	78	8	ATH527607	Sequence	ATH527607	Sequence	C 629	10	34.5	31	6	AX443778	Sequence
C 557	10.2	35.2	78	9	HSU91212	Sequence	HSU91212	Sequence	C 630	10	34.5	31	6	AX443778	Sequence
C 558	10.2	35.2	78	10	MMU543402	Mus muscu	MMU543402	Mus muscu	C 631	10	34.5	31	6	AX443778	Sequence
C 559	10.2	35.2	80	6	AX381967	Sequence	AX381967	Sequence	C 632	10	34.5	31	6	AX443778	Sequence
C 560	10.2	35.2	80	6	AX482376	Sequence	AX482376	Sequence	C 633	10	34.5	31	6	AX443778	Sequence
C 561	10.2	35.2	80	6	AX482379	Sequence	AX482379	Sequence	C 634	10	34.5	31	6	AX443778	Sequence
C 562	10.2	35.2	80	6	AX670713	Sequence	AX670713	Sequence	C 635	10	34.5	31	6	AX443778	Sequence
C 563	10.2	35.2	80	10	RNSC18	Sequence	RNSC18	Sequence	C 636	10	34.5	31	6	AX443778	Sequence
C 564	10.2	35.2	80	11	BN294558	Arabis	BN294558	Arabis	C 637	10	34.5	31	6	AX443778	Sequence
C 565	10.2	35.2	80	11	BN294558	Arabis	BN294558	Arabis	C 638	10	34.5	31	6	AX443778	Sequence
C 566	10.2	35.2	17	6	AX263288	Sequence	AX263288	Sequence	C 639	10	34.5	31	6	AX443778	Sequence
C 567	10.2	35.2	17	6	AX263289	Sequence	AX263289	Sequence	C 640	10	34.5	31	6	AX443778	Sequence
C 568	10.2	35.2	17	6	AX263292	Sequence	AX263292	Sequence	C 641	10	34.5	31	6	AX443778	Sequence
C 569	10.2	35.2	17	6	AX263293	Sequence	AX263293	Sequence	C 642	10	34.5	31	6	AX443778	Sequence
C 570	10.2	35.2	17	6	AX263296	Sequence	AX263296	Sequence	C 643	10	34.5	31	6	AX443778	Sequence
C 571	10.2	35.2	17	6	AX263297	Sequence	AX263297	Sequence	C 644	10	34.5	31	6	AX443778	Sequence
C 572	10.2	35.2	17	6	AX263297	Sequence	AX263297	Sequence	C 645	10	34.5	31	6	AX443778	Sequence
C 573	10.2	35.2	17	6	AX735197	Sequence	AX735197	Sequence	C 646	10	34.5	31	6	AX443778	Sequence
C 574	10.2	35.2	19	6	AX759956	Sequence	AX759956	Sequence	C 647	10	34.5	31	6	AX443778	Sequence
C 575	10.2	35.2	19	6	AX294485	Sequence	AX294485	Sequence	C 648	10	34.5	31	6	AX443778	Sequence
C 576	10.2	35.2	19	6	AX776084	Sequence	AX776084	Sequence	C 649	10	34.5	31	6	AX443778	Sequence
C 577	10.2	35.2	20	6	AX1077	Sequence	AX1077	Sequence	C 650	10	34.5	31	6	AX443778	Sequence

C 650	10	34.5	31	6	AX426157	Sequence	723	10	34.5	57	6	AR128040	Sequence	
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C 654	10	34.5	31	6	BD062977	DNA and B	727	10	34.5	61	6	AR302676	Sequence	
C 655	10	34.5	32	6	A14854	Nucleotide	728	10	34.5	61	6	AX043859	Sequence	
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C 658	10	34.5	33	6	AR306827	Sequence	731	10	34.5	62	10	MUSMAGAL2	Mouse myeli	
C 659	10	34.5	33	6	AX074325	Sequence	732	10	34.5	62	5	AF420500	Salmo sal	
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C 665	10	34.5	35	6	AR103380	Sequence	C	738	10	34.5	65	6	AX486105	Sequence
C 666	10	34.5	35	6	AR169237	Sequence	739	10	34.5	67	6	AX233509	Sequence	
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C 668	10	34.5	35	6	AR216264	Sequence	C	741	10	34.5	67	10	AF265785	Mus muscu
C 669	10	34.5	35	6	AR244352	Sequence	C	742	10	34.5	69	6	AX179410	Sequence
C 670	10	34.5	36	6	AR436550	Sequence	C	743	10	34.5	69	6	AX179437	Sequence
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C 672	10	34.5	37	6	AX465693	Sequence	C	745	10	34.5	69	6	BD036135	Sequence
C 673	10	34.5	38	6	AR046016	Sequence	C	746	10	34.5	69	10	MUSMHTSM	Mus muscu
C 674	10	34.5	38	6	E52281	Ligated glu	C	747	10	34.5	72	8	AXJ59578	Sequence
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C 678	10	34.5	38	6	BD134618	Method fo	C	751	10	34.5	78	6	IO3046	Sequence 13
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C 680	10	34.5	39	6	AX356245	Sequence	C	753	9.8	33.8	16	6	AX362463	Sequence
C 681	10	34.5	40	6	AR034275	Sequence	C	754	9.8	33.8	17	6	A12811	synthetic 1
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C 683	10	34.5	41	6	AX518206	Sequence	C	756	9.8	33.8	17	6	AR433858	Sequence
C 684	10	34.5	41	9	HUMTCVD18U		C	757	9.8	33.8	17	6	AR433859	Sequence
C 685	10	34.5	41	9	S80780	gamma delta	C	758	9.8	33.8	17	6	AR433860	Sequence
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C 693	10	34.5	42	6	BD073227	Growth ho	766	9.8	33.8	17	6	AX732816	Sequence	
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C 699	10	34.5	47	6	AR290933	Sequence	772	9.8	33.8	17	6	AX739798	Sequence	
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C 706	10	34.5	50	6	AR092497	Sequence	779	9.8	33.8	18	6	AR295951	Sequence	
C 707	10	34.5	50	6	AR117221	Sequence	780	9.8	33.8	18	6	BD082090	Reagents	
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C 709	10	34.5	50	6	AR363887	Sequence	C	782	9.8	33.8	19	6	AR293045	Sequence
C 710	10	34.5	51	6	AR157081	Sequence	783	9.8	33.8	19	6	AR294149	Sequence	
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C 719	10	34.5	53	6	AX103641	Sequence	C	792	9.8	33.8	20	6	I73239	Sequence 9
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C 799	9.8	33.8	21	6	AR362466	AR362466 Sequence	C 872	9.8	33.8	30	6	AR048089	AR048089 Sequence
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C 804	9.8	33.8	22	6	E29427	E29427 Oligonucleo	C 877	9.8	33.8	30	6	E58504	E58504 CNTF/IL-6 c
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C 826	9.8	33.8	24	6	AX289155	AX289155 Sequence	C 899	9.8	33.8	30	7	PDPRGMNT2	PDPRGMNT2 Bacterioph
C 827	9.8	33.8	24	6	AX445673	AX445673 Sequence	C 900	9.8	33.8	31	6	BD247621	BD247621 Streptoco
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844	9.8	33.8	26	6	AR309626	AR309626 Sequence	C 917	9.8	33.8	35	11	C75883	C75883 Homo sapien
C 845	9.8	33.8	26	6	AR371892	AR371892 Sequence	C 918	9.8	33.8	36	6	E02235	E02235 Synthetic D
C 846	9.8	33.8	26	6	AR374985	AR374985 Sequence	C 919	9.8	33.8	36	6	AR218089	AR218089 Sequence
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C 866	9.8	33.8	29	6	AX555777	AX555777 Sequence	C 939	9.8	33.8	41	6	AX514585	AX514585 Sequence
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C1000 9.8 33.8 53 6 I06259 Sequence 17

ALIGNMENTS
BD274270 42 bp DNA linear PAT 17-JUL-2003
Identification of molecular interaction sites in RNA for novel drug
discovery.
BD274270.1 GI:33084038
JP 2002526030-A/237.
synthetic construct

RESULT 1
BD274270
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
BD274270.1 GI:33084038
JP 2002526030-A/237
synthetic construct
artificial sequences.
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
Identification of molecular interaction sites in RNA for novel drug
discovery.
Patent: JP 2002526030-A 238 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/238
PD 20-AUG-2002
PP 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/69,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Location/Qualifiers
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUCUUUNNGUAGCCCNANGNG 27
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Db 7 GATTCCTTTGTGAAGCCCTACGGG 30

RESULT 2
BD274271
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
BD274271.1 GI:33084039
JP 2002526030-A/238.
synthetic construct
artificial sequences.
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
Identification of molecular interaction sites in RNA for novel drug
discovery.
Patent: JP 2002526030-A 238 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/238
PD 20-AUG-2002
PP 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/69,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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Best Local Similarity 54.2%; Pred.No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUCUUUNNGUAGCCCNANGNG 27
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Db 7 GATTCCTTTGTGAAGCCCTACGGG 30

RESULT 3
BD274272
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
BD274272.1 GI:33084040
JP 2002526030-A/239.
synthetic construct
artificial sequences.
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
Identification of molecular interaction sites in RNA for novel drug
discovery.
Patent: JP 2002526030-A 239 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/239
PD 20-AUG-2002
PP 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Best Local Similarity 54.2%; Pred.No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Best Local Similarity	54.2%; Pred.No. 5.6;
Matches	13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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7 GATTCTTTTGTAAAGCCCCAAGGG 30	
Db	
RESULT 5	
BD274275	42 bp DNA linear PAT 17-JUL-2003
LOCUS	
DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION	BD274275
VERSION	BD274275.1 GI:33084043
KEYWORDS	JP 2002526030-A/242.
SOURCE	synthetic construct
ORGANISM	artificial construct
REFERENCE	1 (bases 1 to 42)
AUTHORS	Ecker,D.J., Sampath,R., Griffey,R. and Mcneill,J.
TITLE	Identification of molecular interaction sites in RNA for novel drug discovery
JOURNAL	Patient: JP 2002526030-A 242 20-AUG-2002;
COMMENT	ISIS PHARMACEUTICALS INC OS Artificial Sequence PN JP 2002526030-A/242 DP 20-AUG-2002 PP 12-MAY-1999 JP 2000549510 PR 12-MAY-1998 US 60/085092.12-MAY-1998 US 09/076440 PI DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEILL PC C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description of Artificial Sequence: Novel Sequence FH Key
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Matches	13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY	
4 GAUNCUUNNGUAAGCCCNANGNG 27	
7 GATTCTTTTGTAAAGCCCCTAGGG 30	
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RESULT 6	
BD274278	42 bp RNA linear PAT 17-JUL-2003
LOCUS	
DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION	BD274278
VERSION	BD274278.1 GI:33084046
KEYWORDS	JP 2002526030-A/245.

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SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1 (bases 1 to 42)
AUTHORS      Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE        Identification of molecular interaction sites in RNA for novel drug
JOURNAL      discovery
COMMENT      Patent: JP 2002526030-A 245 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002526030-A/245
            PD 20-AUG-2002
            PF 12-MAY-1999 JP 2000548510
            PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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            of Artificial Sequence: Novel Sequence FH Key
            Location/Qualifiers
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Best Local Similarity 54.2%; Pred. No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
Db 7 GATTCCTTTTGTAGCCCTACGGG 30
RESULT 7
BD274279
LOCUS      42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274279
VERSION    1 GI:33084047
KEYWORDS   JP 2002526030-A/246.
SOURCE     synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 42)
AUTHORS     Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE       Identification of molecular interaction sites in RNA for novel drug
JOURNAL     discovery
COMMENT     Patent: JP 2002526030-A 246 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002526030-A/246
            PD 20-AUG-2002
            PF 12-MAY-1999 JP 2000548510
            PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Best Local Similarity 54.2%; Pred. No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
Db 7 GATTCCTTTTGTAGCCCTACGGG 30

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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
Db 7 GATTCCTTTTGTAGCCCTACGGG 30
RESULT 8
BD274280
LOCUS      42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274280
VERSION    1 GI:33084048
KEYWORDS   JP 2002526030-A/247.
SOURCE     synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 42)
AUTHORS     Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE       Identification of molecular interaction sites in RNA for novel drug
JOURNAL     discovery
COMMENT     Patent: JP 2002526030-A 247 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002526030-A/247
            PD 20-AUG-2002
            PF 12-MAY-1999 JP 2000548510
            PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
            of Artificial Sequence: Novel Sequence FH Key
            Location/Qualifiers
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Db 7 GATTCCTTTTGTAGCCCTACGGG 30
RESULT 9
BD274281
LOCUS      42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274281
VERSION    1 GI:33084049
KEYWORDS   JP 2002526030-A/248.
SOURCE     synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 42)
AUTHORS     Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE       Identification of molecular interaction sites in RNA for novel drug
JOURNAL     discovery
COMMENT     Patent: JP 2002526030-A 248 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002526030-A/248
            PD 20-AUG-2002
            PF 12-MAY-1999 JP 2000548510
            PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI

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Db 8 GATNCITTTNGTAAGCCCNANGNG 31
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RESULT 13
BD274238 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274238
VERSION BD274238.1 GI:33084006
KEYWORDS JP 2002526030-A/205.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT Patent: JP 2002526030-A 205 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/205
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Best Local Similarity 62.1%; Score 18; DB 6; Length 46;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 22 GATTCITTTTGTAGCCCTACGGG 45
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RESULT 14
BD274240 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274240
VERSION BD274240.1 GI:33084009
KEYWORDS JP 2002526030-A/208.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT Patent: JP 2002526030-A 208 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/208
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 22 GATTCITTTTGTAGCCCTACGGG 45
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Dd	22 GATCTTTTGTAAAGCCTACGGG	45		
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RESULT 18				
BD274246				
LOCUS	BD274246	46 bp	DNA	linear PAT 17-JUL-2003
DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.			
ACCESSION	BD274246			
VERSION	BD274246.1	G1:33084014		
KEYWORDS	JP 2002526030-A/213.			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 46)			
AUTHORS	Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.			
TITLE	Identification of molecular interaction sites in RNA for novel drug discovery			
JOURNAL	Patent: JP 2002526030-A 213 20-AUG-2002;			
COMMENT	ISIS PHARMACEUTICALS INC			
	OS	Artificial Sequence		
	PN	JP 2002526030-A/213		
	PD	20-AUG-2002		
	PF	12-MAY-1999 JP	2000548510	
	PR	12-MAY-1998 US	60/085092,12-MAY-1998 US	09/076440 PI
	DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC			
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Dd	22 GATCTTTTGTAAAGCCTACGGG	45		
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RESULT 19				
BD274247				
LOCUS	BD274247	46 bp	DNA	linear PAT 17-JUL-2003
DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.			

Query Match	62.1%;	Score 18;	DB 6;	Length 46;
Best Local Similarity	54.2%;	Pred. No. 5.6;		
Matches	13;	Conservative	5;	Mismatches 6; Indels 0; Gaps 0;
QY	4	GAUNCUUUNNGUAAGCCCNANGNG	27	
Db	22	GATCCTTTCTGTAAGCCCTACGGG	45	
RESULT 21				
BD274249				
LOCUS		46 bp	DNA	linear
DEFINITION		Identification of molecular interaction sites in RNA for novel drug discovery.		
ACCESSION		BD274249		
VERSION		BD274249.1		GI:33084017
KEYWORDS		JP 2002526030-A/216.		
SOURCE		synthetic construct		
ORGANISM		synthetic construct		
		artificial sequences.		
REFERENCE		1 (bases 1 to 46)		
AUTHORS		Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.		
TITLE		Identification of molecular interaction sites in RNA for novel drug discovery		
JOURNAL		Patent: JP 2002526030-A 216 20-AUG-2002;		
COMMENT		ISIS PHARMACEUTICALS INC		
		OS Artificial Sequence		
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		PD 20-AUG-2002		
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LOCUS		46 bp	DNA	linear
DEFINITION		Identification of molecular interaction sites in RNA for novel drug discovery.		
ACCESSION		BD274252		
VERSION		BD274252.1		GI:33084020
KEYWORDS		JP 2002526030-A/219.		
SOURCE		synthetic construct		
ORGANISM		synthetic construct		
		artificial sequences.		
REFERENCE		1 (bases 1 to 46)		
AUTHORS		Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.		
TITLE		Identification of molecular interaction sites in RNA for novel drug discovery		
JOURNAL		Patent: JP 2002526030-A 219 20-AUG-2002;		
COMMENT		ISIS PHARMACEUTICALS INC		
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		FN JP 2002526030-A/219		


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DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274262
VERSION BD274262.1 GI:33084030
KEYWORDS JP 2002526030-A/229.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 229 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/229
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 22 GATCCTTCTGTAGCCCTACGGG 45

RESULT 30
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LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274263
VERSION BD274263.1 GI:33084031
KEYWORDS JP 2002526030-A/230.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 230 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/230
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Db 22 GATCCTTCTGTAGCCCTACGGG 45

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BD274264
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274264
VERSION BD274264.1 GI:33084032
KEYWORDS JP 2002526030-A/231.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 231 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/231
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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Best Local Similarity 54.2%; Pred. No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 22 GATCCTTCTGTAGCCCTACGGG 45

RESULT 32
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LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274265
VERSION BD274265.1 GI:33084033
KEYWORDS JP 2002526030-A/232.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 232 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274264
VERSION BD274264.1 GI:33084032
KEYWORDS JP 2002526030-A/231.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 231 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/231
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 22 GATCCTTCTGTAGCCCTACGGG 45

RESULT 32
BD274265
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274265
VERSION BD274265.1 GI:33084033
KEYWORDS JP 2002526030-A/232.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 232 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
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ACCESSION BD274251
VERSION    1 GI:33084019
KEYWORDS   JP 2002526030-A/218.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 46)
AUTHORS    Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE      Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL    Patent: JP 2002526030-A 218 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/218
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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FH Key Location/Qualifiers
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Query Match          51.7%; Score 15; DB 6; Length 46;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNGUAGGCC 21
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Db 22 GATTCCTTTTGTGAAGCC 39

RESULT 36
BD274251
LOCUS      46 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274251
VERSION    1 GI:33084019
KEYWORDS   JP 2002526030-A/218.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 46)
AUTHORS    Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE      Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL    Patent: JP 2002526030-A 218 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/218
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
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Query Match          51.7%; Score 15; DB 6; Length 46;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNGUAGGCC 21
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Db 22 GATTCCTTTTGTGAAGCC 39

RESULT 37
BD274255
LOCUS      46 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274255
VERSION    1 GI:33084023
KEYWORDS   JP 2002526030-A/222.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 46)
AUTHORS    Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE      Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL    Patent: JP 2002526030-A 222 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence

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ACCESSION BD274276
VERSION BD274276.1 GI:33084044
KEYWORDS JP 2002526030-A/243.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT
PATENT: JP 2002526030-A 243 20-AUG-2002;
OS Artificial Sequence
PN JP 2002526030-A/243
PD 20-AUG-2002 JP 2000548510
PR 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Location/Qualifiers
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RESULT 40
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LOCUS
DEFINITION 42 bp DNA linear PAT 17-JUL-2003
Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274274
VERSION BD274274.1 GI:33084042
KEYWORDS JP 2002526030-A/241.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT
PATENT: JP 2002526030-A 241 20-AUG-2002;
OS Artificial Sequence
PN JP 2002526030-A/241
PD 20-AUG-2002 JP 2000548510
PR 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence PH Key
Location/Qualifiers
FT source 1..42
FT Location/Qualifiers
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Best Local Similarity 55.6%; Pred. No. 9e+03;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 10 UUNNGUAGCCNANGNG 27
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Db 13 TTTTGTAGCCCTAAGGG 30

Search completed: April 18, 2004, 08:41:04
Job time : 775.333 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:05:34 ; Search time 179.667 Seconds
(without alignments)
685.702 Million cell updates/sec

Title: US-09-310-844C-23

Perfect score: 29

Sequence: 1 nngauncuunnguaagcccnangnngn 29

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Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3399856

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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28	18	62.1	46	3	AAA71089	AAA71089	Molecular
29	18	62.1	46	3	AAA71094	AAA71094	Molecular
30	18	62.1	46	3	AAA71085	AAA71085	Molecular
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36	18	62.1	46	3	AAA71109	AAA71109	Molecular
37	18	62.1	46	3	AAA71087	AAA71087	Molecular
38	18	62.1	46	3	AAA71093	AAA71093	Molecular
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61	12.2	42.1	55	2	AAQ37152	AAQ37152	Probe to
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63	12.2	42.1	60	6	ABN39439	ABN39439	Human spl
64	12.2	42.1	60	6	ABN46186	ABN46186	Human spl
65	12.2	42.1	60	6	ABN42361	ABN42361	Human spl
66	12.2	42.1	69	2	AAV08003	AAV08003	Probe II-
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113	11.4	39.3	17	7	ABT34657	Abt34657 Tumour su	c 186	11.2	38.6	50	6	ABZ06777	Abz06777 Human leu
114	11.4	39.3	20	2	AAZ04979	Aaz04979 PCR prime	c 187	11.2	38.6	50	6	ABZ07461	Abz07461 Human leu
115	11.4	39.3	25	8	ACI05200	AcI05200 Human mic	c 188	11.2	38.6	51	4	AAI31644	Aai31644 Human SNP
116	11.4	39.3	25	8	ACI05201	AcI05201 Human mic	c 189	11.2	38.6	51	4	AAI26911	Aai26911 Human SNP
117	11.4	39.3	25	8	ACI94430	AcI94430 Human mic	c 190	11.2	38.6	52	2	AAV69331	Aav69331 Human LIR
118	11.4	39.3	31	3	AAZ87592	Aaz87592 Mouse CD1	c 191	11.2	38.6	52	3	AA545594	Aa545594 Primer us
119	11.4	39.3	31	3	AAZ87589	Aaz87589 Human CD1	c 192	11.2	38.6	56	4	AA509291	Aas09291 RNA seque
120	11.4	39.3	36	2	AAZ47031	Aat47031 CD40 liga	c 193	11.2	38.6	60	1	AAZ70575	Aan70575 Coliphage
121	11.4	39.3	40	6	ABD27069	Abd27069 Plasmid p	c 194	11.2	38.6	60	6	ABN49506	Abn49506 Human spl
122	11.4	39.3	41	6	AB154588	Ab154588 Human pro	c 195	11.2	38.6	60	6	ABN47240	Abn47240 Human spl
123	11.4	39.3	44	3	AAZ71108	Aaz71108 Molecular	c 196	11.2	38.6	60	6	ABN47240	Abn47240 Human spl
124	11.4	39.3	44	4	AAZ82920	Aaz82920 CD154 ext	c 197	11.2	38.6	65	6	ABN30679	Abn30679 Rat splic
125	11.4	39.3	44	4	ABX89864	Abx89864 Binding d	c 198	11.2	38.6	65	6	ABN31177	Abn31177 Rat splic
126	11.4	39.3	44	9	ADD25467	Add25467 Binding d	c 199	11.2	38.6	65	6	ABN31177	Abn31177 Rat splic
127	11.4	39.3	46	3	AAA71092	Aaa71092 Molecular	c 200	11.2	38.6	70	5	AAF29242	Aaf29242 Ligand to
128	11.4	39.3	46	6	ABN72001	Abn72001 Streptoco	c 201	11.2	38.6	70	9	ADC64809	Adc64809 HUBBK-4H-
129	11.4	39.3	49	6	ABN71758	Abn71758 Human SNP	c 202	11.2	38.6	78	9	ABE85488	Abe85488 Farnesyl
130	11.4	39.3	49	6	ABN46181	Abn46181 ccdB gene	c 203	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
131	11.4	39.3	51	4	AAZ29026	Aaz29026 Human DNA	c 204	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
132	11.4	39.3	51	4	AAH79850	Aah79850 Human DNA	c 205	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
133	11.4	39.3	60	6	ABK36336	Abk36336 HIV DNA e	c 206	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
134	11.4	39.3	60	6	ABN47785	Abn47785 Human spl	c 207	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
135	11.4	39.3	60	6	ABN33454	Abn33454 Human spl	c 208	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
136	11.4	39.3	60	6	ABN35172	Abn35172 Human spl	c 209	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
137	11.4	39.3	65	2	AAV36558	Aav36558 DNA subet	c 210	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
138	11.4	39.3	65	6	ABN31992	Abn31992 Rat splic	c 211	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
139	11.2	38.6	20	6	AB193874	Ab193874 Capture o	c 212	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
140	11.2	38.6	24	6	AB184319	Ab184319 Capture o	c 213	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
141	11.2	38.6	24	6	AB192761	Ab192761 Capture o	c 214	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
142	11.2	38.6	24	6	AB182565	Ab182565 Capture o	c 215	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
143	11.2	38.6	24	6	AB184318	Ab184318 Capture o	c 216	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
144	11.2	38.6	24	6	AB192760	Ab192760 Capture o	c 217	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
145	11.2	38.6	24	6	AB191830	Ab191830 Capture o	c 218	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
146	11.2	38.6	24	6	AB182564	Ab182564 Capture o	c 219	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
147	11.2	38.6	24	6	AB191831	Ab191831 Capture o	c 220	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
148	11.2	38.6	24	8	ACF04473	Acf04473 Real time	c 221	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
149	11.2	38.6	25	3	AAZ29218	Aaz29218 Sindbis v	c 222	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
150	11.2	38.6	25	3	AAZ29219	Aaz29219 Sindbis v	c 223	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
151	11.2	38.6	25	3	AAZ292791	Aaz292791 Sindbis v	c 224	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
152	11.2	38.6	25	6	ABK46284	Abk46284 Viral min	c 225	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
153	11.2	38.6	25	8	ACK00386	Ack00386 Human mic	c 226	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
154	11.2	38.6	25	8	ACK137324	Ack137324 Human mic	c 227	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
155	11.2	38.6	25	8	ACK30015	Ack30015 Human mic	c 228	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
156	11.2	38.6	30	2	AAQ70868	Aaq70868 Target se	c 229	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
157	11.2	38.6	30	2	ABX69578	Abx69578 Novel Hel	c 230	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
158	11.2	38.6	32	4	AAF86171	Aaf86171 Rat thior	c 231	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
159	11.2	38.6	33	3	AAZ29219	Aaz29219 Sindbis v	c 232	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
160	11.2	38.6	33	3	AAZ292792	Aaz292792 Sindbis v	c 233	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
161	11.2	38.6	33	6	AAI38799	Aai38799 Alphaviru	c 234	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
162	11.2	38.6	33	6	ABK46265	Abk46265 Viral min	c 235	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
163	11.2	38.6	34	2	AAV90805	Aav90805 Primer Y2	c 236	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
164	11.2	38.6	34	2	AAV02487	Aav02487 Bridge MP	c 237	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
165	11.2	38.6	36	2	AAV02466	Aav02466 Primer MP	c 238	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
166	11.2	38.6	36	2	AAV02466	Aav02466 Primer MP	c 239	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
167	11.2	38.6	36	4	AAAC81683	Aaac81683 Chimeric	c 240	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
168	11.2	38.6	37	9	ADC24312	Adc24312 PCR prime	c 241	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su
169	11.2	38.6	37	9	ADC24311	Adc24311 ERI prime	c 242	11.2	38.6	78	9	ABT35710	Abt35710 Tumour su

c 243	10.8	37.2	22	5	ABQ88570	Abq88570 Human GPC	316	10.8	37.2	60	6	ABN50045	Abn50045 Human spl
c 244	10.8	37.2	23	3	AAQ99238	Aaa99238 Human pho	c 317	10.8	37.2	60	6	ABN42062	Abn42062 Human spl
c 245	10.8	37.2	24	3	ACF03497	Acf03497 Oryza sat	c 318	10.8	37.2	60	6	ABN36609	Abn36609 Human spl
c 246	10.8	37.2	25	4	AAV90566	Aav90566 Forward p	c 319	10.8	37.2	60	6	ABN32506	Abn32506 Human spl
c 247	10.8	37.2	25	4	AAV39727	Aav39727 SNP speci	c 320	10.8	37.2	61	2	AAV76047	Aav76047 Staphyloc
c 248	10.8	37.2	25	5	AA522104	Aas22104 Human COL	c 321	10.8	37.2	64	7	ABZ17788	Abz17788 S2 subtra
c 249	10.8	37.2	25	6	AB575571	Ab575571 Human PAP	c 322	10.8	37.2	65	6	ABZ29118	Abz29118 Candida g
c 250	10.8	37.2	25	6	AB575578	Ab575578 Human PAP	c 323	10.8	37.2	65	6	ABZ29526	Abz29526 Candida g
c 251	10.8	37.2	25	6	AB575577	Ab575577 Human PAP	c 324	10.8	37.2	65	6	ABZ26621	Abz26621 Candida e
c 252	10.8	37.2	25	6	AB575572	Ab575572 Human PAP	c 325	10.8	37.2	65	6	ABN57271	Abn57271 Mouse spl
c 253	10.8	37.2	25	6	AB575576	Ab575576 Human PAP	c 326	10.8	37.2	65	6	ABN57807	Abn57807 Mouse spl
c 254	10.8	37.2	25	6	AB575574	Ab575574 Human PAP	c 327	10.8	37.2	65	6	ABN56758	Abn56758 Mouse spl
c 255	10.8	37.2	25	6	AB575575	Ab575575 Human PAP	c 328	10.6	36.6	23	2	AA101534	Aat01534 Human her
c 256	10.8	37.2	25	8	ACK80900	Ack80900 Human mic	c 329	10.6	36.6	23	2	AA103719	Aat03719 Human her
c 257	10.8	37.2	25	8	ACK80900	Ack80900 Human mic	c 330	10.6	36.6	24	3	AAZ35966	Aaz35966 Cytochrom
c 258	10.8	37.2	25	8	AC165128	Ac165128 Human mic	c 331	10.6	36.6	24	3	ABT31746	Abt31746 IRF1 p53
c 259	10.8	37.2	25	8	AC153509	Ac153509 Human mic	c 332	10.6	36.6	25	8	AC171263	Ac171263 Human mic
c 260	10.8	37.2	25	8	ACK38091	Ack38091 Human mic	c 333	10.6	36.6	25	8	AC132666	Ac132666 Human mic
c 261	10.8	37.2	25	8	ACH52985	Ach52985 DNA targe	c 334	10.6	36.6	25	8	AC195082	Ac195082 Human mic
c 262	10.8	37.2	27	2	AAZ27163	Aaz27163 Caenorhab	c 335	10.6	36.6	25	8	ACK06797	Ack06797 Human mic
c 263	10.8	37.2	27	4	AAH38439	Aah38439 SNP speci	c 336	10.6	36.6	25	8	AC101290	Ac101290 Human mic
c 264	10.8	37.2	29	3	AAA42116	Aaa42116 Polymorph	c 337	10.6	36.6	25	8	AC101291	Ac101291 Human mic
c 265	10.8	37.2	29	3	AAAI0646	Aaa10646 PCR prime	c 338	10.6	36.6	28	3	AAA40375	Aaa40375 Feline fo
c 266	10.8	37.2	30	9	ADL54532	Adc5106 Primer #1	c 339	10.6	36.6	29	2	AAQ43929	Aaq43929 Primer BL
c 267	10.8	37.2	32	9	ADC58048	Adc58048 PCR prime	c 340	10.6	36.6	29	3	AAA04444	Aaa04444 Polymorph
c 268	10.8	37.2	33	6	ABL54520	Ab154520 Pectinatu	c 341	10.6	36.6	29	7	ACC59203	Acc59203 Human ade
c 269	10.8	37.2	33	7	ACC00085	Acc00085 Primer #4	c 342	10.6	36.6	29	7	ACC59205	Acc59205 Human ade
c 270	10.8	37.2	33	9	ADB92927	Adb92927 PCR prime	c 343	10.6	36.6	30	2	AXX28008	Axx28008 E3L RNA b
c 271	10.8	37.2	35	2	AXX99670	Axx99670 Reverse p	c 344	10.6	36.6	30	2	AAZ30456	Aaz30456 Primer 9
c 272	10.8	37.2	40	3	AAAS1108	Aaa51108 Oligomer	c 345	10.6	36.6	30	4	AXC89507	Axc89507 Soybean p
c 273	10.8	37.2	40	6	ABL54532	Ab154532 Pectinatu	c 346	10.6	36.6	30	6	ABX69591	Abx69591 Novel Hel
c 274	10.8	37.2	40	6	ABK93286	Abk93286 Human ser	c 347	10.6	36.6	30	9	ADB85428	Adb85428 PCR prime
c 275	10.8	37.2	41	3	AAAY70544	Aaa70544 Reverse p	c 348	10.6	36.6	31	4	ABL48203	Ab148203 Human GRI
c 276	10.8	37.2	41	6	ABZ48930	Abz48930 Human ald	c 349	10.6	36.6	31	4	ABL48019	Ab148019 Human GRI
c 277	10.8	37.2	41	6	ABZ46418	Abz46418 Human ald	c 350	10.6	36.6	31	4	ABL48014	Ab148014 Human GRI
c 278	10.8	37.2	42	6	ABK93317	Abk93317 Human 5-h	c 351	10.6	36.6	31	6	ABK21667	Abk21667 Human ERG
c 279	10.8	37.2	43	6	ABZ27920	Abz27920 Candida e	c 352	10.6	36.6	31	6	ABK21707	Abk21707 Human ERG
c 280	10.8	37.2	45	2	AAQ69592	Aaq69592 Human gen	c 353	10.6	36.6	31	6	ABK21754	Abk21754 Human ERG
c 281	10.8	37.2	45	2	AAQ69380	Aaq69380 Human fib	c 354	10.6	36.6	31	6	ABK21513	Abk21513 Human ERG
c 282	10.8	37.2	45	2	AAQ64054	Aat64054 Human fib	c 355	10.6	36.6	31	6	ABK60174	Abk60174 Human CLC
c 283	10.8	37.2	45	2	AAT63842	Aat63842 Human fib	c 356	10.6	36.6	31	6	ABK59880	Abk59880 Human CLC
c 284	10.8	37.2	45	2	AAT63842	Aat63842 Human fib	c 357	10.6	36.6	31	6	ABK60180	Abk60180 Human CLC
c 285	10.8	37.2	45	2	AAI17130	Aai17130 Test sequ	c 358	10.6	36.6	31	6	ABK59976	Abk59976 Human CLC
c 286	10.8	37.2	45	2	AAI17342	Aai17342 Test sequ	c 359	10.6	36.6	31	6	ABK60209	Abk60209 Human CLC
c 287	10.8	37.2	45	6	ABK92833	Abk92833 DNA bindi	c 360	10.6	36.6	31	7	ACA08645	AcA08645 Necrosin
c 288	10.8	37.2	45	6	ABK92621	Abk92621 DNA bindi	c 361	10.6	36.6	31	7	ABZ66333	Abz66333 Human HER
c 289	10.8	37.2	45	9	ADC33438	Adc33438 Rat p60R	c 362	10.6	36.6	31	7	ABZ66068	Abz66068 Human HER
c 290	10.8	37.2	45	10	ADB80160	Adb80160 Duplex ol	c 363	10.6	36.6	31	7	ABZ66068	Abz66068 Human HER
c 291	10.8	37.2	45	10	ADB80372	Adb80372 Duplex ol	c 364	10.6	36.6	31	7	ABZ65632	Abz65632 Human HER
c 292	10.8	37.2	47	3	AAZ67939	Aaz67939 Human map	c 365	10.6	36.6	31	7	ABZ65797	Abz65797 Human HER
c 293	10.8	37.2	48	2	AAI02929	Aai02929 Human glu	c 366	10.6	36.6	31	7	ABZ63906	Abz63906 Human H-R
c 294	10.8	37.2	50	2	AAQ69593	Aaq69593 Human gen	c 367	10.6	36.6	31	7	ABZ62376	Abz62376 Human K-R
c 295	10.8	37.2	50	2	AAT64055	Aat64055 Human gen	c 368	10.6	36.6	31	7	ABZ64179	Abz64179 Human H-R
c 296	10.8	37.2	50	2	AAI17343	Aai17343 Test sequ	c 369	10.6	36.6	31	7	ABZ66071	Abz66071 Human HER
c 297	10.8	37.2	50	3	AAAS1146	Aaa51146 Oligomer	c 370	10.6	36.6	31	7	ACD62205	AcD62205 HCV minus
c 298	10.8	37.2	50	3	AAZ29462	Aaz29462 PCR prime	c 371	10.6	36.6	31	7	ACD59882	AcD59882 HCV DNaz
c 299	10.8	37.2	50	3	AAI28930	Aai28930 Human SNP	c 372	10.6	36.6	31	7	ACD61654	AcD61654 HCV minus
c 300	10.8	37.2	50	6	ABK82834	Abk82834 DNA bindi	c 373	10.6	36.6	31	7	ACD57211	AcD57211 HCV DNaz
c 301	10.8	37.2	50	6	ABZ01498	Abz01498 Human leu	c 374	10.6	36.6	31	7	ACD59572	AcD59572 HCV minus
c 302	10.8	37.2	50	6	ABZ03691	Abz03691 Human leu	c 375	10.6	36.6	31	7	ACD65339	AcD65339 HCV minus
c 303	10.8	37.2	50	6	ABZ02255	Abz02255 Human leu	c 376	10.6	36.6	31	7	ACD62869	AcD62869 HCV minus
c 304	10.8	37.2	50	10	ADB80373	Adb80373 Duplex ol	c 377	10.6	36.6	31	7	ACD54958	AcD54958 HCV DNaz
c 305	10.8	37.2	51	4	AAI26990	Aai26990 Human SNP	c 378	10.6	36.6	31	7	ACD60482	AcD60482 HCV DNaz
c 306	10.8	37.2	51	4	AAH90685	Aah90685 Human CLO	c 379	10.6	36.6	33	6	ABK14720	Abk14720 Pogo conv
c 307	10.8	37.2	51	4	AAH39728	Aah39728 Human SNP	c 380	10.6	36.6	33	6	AAI47565	Aai47565 Human pur
c 308	10.8	37.2	51	4	AAH40360	Aah40360 Human SNP	c 381	10.6	36.6	33	6	ABL55338	Ab155338 Human RNA
c 309	10.8	37.2	51	6	AB198852	Ab198852 Oligonuc	c 382	10.6	36.6	34	9	ADC40550	Adc40550 Replicati
c 310	10.8	37.2	60	6	ABN50311	Abn50311 Human spl	c 383	10.6	36.6	35	4	AAI13700	Aai13700 Arabidops
c 311	10.8	37.2	60	6	ABN42592	Abn42592 Human spl	c 384	10.6	36.6	38	2	AAV07069	Aav07069 Degenerat
c 312	10.8	37.2	60	6	ABN42592	Abn42592 Human spl	c 385	10.6	36.6	39	7	ABX99212	Abx99212 Human CAN
c 313	10.8	37.2	60	6	ABN47524	Abn47524 Human spl	c 386	10.6	36.6	40	7	ABZ72385	Abz72385 Tomato.sp
c 314	10.8	37.2	60	6	ABN41771	Abn41771 Human spl	c 387	10.6	36.6	41	2	AAQ98959	Aaq98959 PUC 525 p
c 315	10.8	37.2	60	6	ABN45568	Abn45568 Human spl	c 388	10.6	36.6	41	6	ABV72968	Abv72968 Human FW

C 389	10.6	36.6	41	6	ABZ50144	Abz50144 Human NDU	462	10.4	35.9	25	8	ACI49963	Human mic
C 390	10.6	36.6	41	6	ABZ44134	Abz44134 Human NDU	463	10.4	35.9	26	2	AAI71933	Primer de
C 391	10.6	36.6	43	6	ABL51319	AbL51319 Bacteriop	464	10.4	35.9	26	2	AAI72005	Primer de
C 392	10.6	36.6	43	6	ABL51317	AbL51317 Bacteriop	465	10.4	35.9	27	3	AAZ32859	LacCoccc
C 393	10.6	36.6	47	3	AZ67926	Az67926 Human map	466	10.4	35.9	27	5	AAZ32859	LacCoccc
C 394	10.6	36.6	47	3	AZ67926	Az67926 Human map	467	10.4	35.9	27	5	AAZ32859	LacCoccc
C 395	10.6	36.6	50	6	ABZ00247	Abz00247 Human leu	468	10.4	35.9	27	6	ABN85152	Abn85152 HIV gp41
C 396	10.6	36.6	50	6	ABZ00247	Abz00247 Human leu	469	10.4	35.9	27	6	ABN85152	Abn85152 HIV gp41
C 397	10.6	36.6	50	6	ABZ00247	Abz00247 Human leu	470	10.4	35.9	27	6	ABN85152	Abn85152 HIV gp41
C 398	10.6	36.6	50	6	ABZ00247	Abz00247 Human leu	471	10.4	35.9	27	6	ABN85152	Abn85152 HIV gp41
C 399	10.6	36.6	51	2	AAI28434	AaI28434 Human SNP	472	10.4	35.9	29	2	AAI79720	Immunoglo
C 400	10.6	36.6	51	2	AAI28434	AaI28434 Human SNP	473	10.4	35.9	29	2	AAI79720	Immunoglo
C 401	10.6	36.6	52	4	AAI28434	AaI28434 Human SNP	474	10.4	35.9	29	2	AAI79720	Immunoglo
C 402	10.6	36.6	53	7	ABX54825	Abx54825 Bovine ES	475	10.4	35.9	29	2	AAI79720	Immunoglo
C 403	10.6	36.6	54	2	AAI43638	AaI43638 HIV-1 mat	476	10.4	35.9	29	2	AAI79720	Immunoglo
C 404	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	477	10.4	35.9	29	2	AAI79720	Immunoglo
C 405	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	478	10.4	35.9	29	2	AAI79720	Immunoglo
C 406	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	479	10.4	35.9	29	2	AAI79720	Immunoglo
C 407	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	480	10.4	35.9	29	2	AAI79720	Immunoglo
C 408	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	481	10.4	35.9	29	2	AAI79720	Immunoglo
C 409	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	482	10.4	35.9	29	2	AAI79720	Immunoglo
C 410	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	483	10.4	35.9	29	2	AAI79720	Immunoglo
C 411	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	484	10.4	35.9	29	2	AAI79720	Immunoglo
C 412	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	485	10.4	35.9	29	2	AAI79720	Immunoglo
C 413	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	486	10.4	35.9	29	2	AAI79720	Immunoglo
C 414	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	487	10.4	35.9	29	2	AAI79720	Immunoglo
C 415	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	488	10.4	35.9	29	2	AAI79720	Immunoglo
C 416	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	489	10.4	35.9	29	2	AAI79720	Immunoglo
C 417	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	490	10.4	35.9	29	2	AAI79720	Immunoglo
C 418	10.6	36.6	63	4	AAK96512	AaK96512 Human neu	491	10.4	35.9	29	2	AAI79720	Immunoglo
C 419	10.6	36.6	64	4	AAK98005	AaK98005 Human neu	492	10.4	35.9	29	2	AAI79720	Immunoglo
C 420	10.6	36.6	64	4	AAK98005	AaK98005 Human neu	493	10.4	35.9	29	2	AAI79720	Immunoglo
C 421	10.6	36.6	64	4	AAK98005	AaK98005 Human neu	494	10.4	35.9	29	2	AAI79720	Immunoglo
C 422	10.6	36.6	64	4	AAK98005	AaK98005 Human neu	495	10.4	35.9	29	2	AAI79720	Immunoglo
C 423	10.6	36.6	64	4	AAK98005	AaK98005 Human neu	496	10.4	35.9	29	2	AAI79720	Immunoglo
C 424	10.6	36.6	65	6	ABZ28932	Abz28932 Candida g	497	10.4	35.9	29	2	AAI79720	Immunoglo
C 425	10.6	36.6	65	6	ABZ28932	Abz28932 Candida g	498	10.4	35.9	29	2	AAI79720	Immunoglo
C 426	10.6	36.6	65	6	ABZ28932	Abz28932 Candida g	499	10.4	35.9	29	2	AAI79720	Immunoglo
C 427	10.6	36.6	65	6	ABZ28932	Abz28932 Candida g	500	10.4	35.9	29	2	AAI79720	Immunoglo
C 428	10.6	36.6	65	6	ABZ28932	Abz28932 Candida g	501	10.4	35.9	29	2	AAI79720	Immunoglo
C 429	10.6	36.6	66	8	AAI62774	AaI62774 Escherich	502	10.4	35.9	29	2	AAI79720	Immunoglo
C 430	10.6	36.6	66	8	AAI62774	AaI62774 Escherich	503	10.4	35.9	29	2	AAI79720	Immunoglo
C 431	10.6	36.6	69	4	AAI21265	AaI21265 Interleuk	504	10.4	35.9	29	2	AAI79720	Immunoglo
C 432	10.6	36.6	69	4	AAI21265	AaI21265 Interleuk	505	10.4	35.9	29	2	AAI79720	Immunoglo
C 433	10.6	36.6	69	4	AAI21265	AaI21265 Interleuk	506	10.4	35.9	29	2	AAI79720	Immunoglo
C 434	10.6	36.6	70	3	ABK02859	Abk02859 Human sec	507	10.4	35.9	29	2	AAI79720	Immunoglo
C 435	10.4	35.9	17	4	ABK03226	Abk03226 Human CD2	508	10.4	35.9	29	2	AAI79720	Immunoglo
C 436	10.4	35.9	17	4	ABK03226	Abk03226 Human CD2	509	10.4	35.9	29	2	AAI79720	Immunoglo
C 437	10.4	35.9	17	4	ABK03226	Abk03226 Human CD2	510	10.4	35.9	29	2	AAI79720	Immunoglo
C 438	10.4	35.9	17	6	ABK92273	Abk92273 Human GST	511	10.4	35.9	29	2	AAI79720	Immunoglo
C 439	10.4	35.9	17	7	ACD50361	AcD50361 HBV inoz	512	10.4	35.9	29	2	AAI79720	Immunoglo
C 440	10.4	35.9	17	7	ACD50361	AcD50361 HBV inoz	513	10.4	35.9	29	2	AAI79720	Immunoglo
C 441	10.4	35.9	17	7	ACD50361	AcD50361 HBV inoz	514	10.4	35.9	29	2	AAI79720	Immunoglo
C 442	10.4	35.9	18	4	AAI79720	AaI79720 PCR prime	515	10.4	35.9	29	2	AAI79720	Immunoglo
C 443	10.4	35.9	20	2	AAI79720	AaI79720 PCR prime	516	10.4	35.9	29	2	AAI79720	Immunoglo
C 444	10.4	35.9	20	3	AAI79720	AaI79720 PCR prime	517	10.4	35.9	29	2	AAI79720	Immunoglo
C 445	10.4	35.9	20	4	AAI79720	AaI79720 PCR prime	518	10.4	35.9	29	2	AAI79720	Immunoglo
C 446	10.4	35.9	20	7	AAI79720	AaI79720 PCR prime	519	10.4	35.9	29	2	AAI79720	Immunoglo
C 447	10.4	35.9	21	2	AAI79720	AaI79720 PCR prime	520	10.4	35.9	29	2	AAI79720	Immunoglo
C 448	10.4	35.9	21	2	AAI79720	AaI79720 PCR prime	521	10.4	35.9	29	2	AAI79720	Immunoglo
C 449	10.4	35.9	22	2	AAI79720	AaI79720 PCR prime	522	10.4	35.9	29	2	AAI79720	Immunoglo
C 450	10.4	35.9	22	2	AAI79720	AaI79720 PCR prime	523	10.4	35.9	29	2	AAI79720	Immunoglo
C 451	10.4	35.9	24	9	ADZ64604	Adz64604 Somatosta	524	10.4	35.9	29	2	AAI79720	Immunoglo
C 452	10.4	35.9	24	9	ADZ64604	Adz64604 Somatosta	525	10.4	35.9	29	2	AAI79720	Immunoglo
C 453	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	526	10.4	35.9	29	2	AAI79720	Immunoglo
C 454	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	527	10.4	35.9	29	2	AAI79720	Immunoglo
C 455	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	528	10.4	35.9	29	2	AAI79720	Immunoglo
C 456	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	529	10.4	35.9	29	2	AAI79720	Immunoglo
C 457	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	530	10.4	35.9	29	2	AAI79720	Immunoglo
C 458	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	531	10.4	35.9	29	2	AAI79720	Immunoglo
C 459	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	532	10.4	35.9	29	2	AAI79720	Immunoglo
C 460	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	533	10.4	35.9	29	2	AAI79720	Immunoglo
C 461	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	534	10.4	35.9	29	2	AAI79720	Immunoglo

C 535	10.4	35.9	60	6	ABN40128	Human spl	Abn40128	Human spl	C 608	10.2	35.2	25	8	ACI80480	Human mic
536	10.4	35.9	60	6	ABN43390	Human spl	Abn43390	Human spl	609	10.2	35.2	25	8	ACI82304	Human mic
537	10.4	35.9	60	6	ABN49374	Human spl	Abn49374	Human spl	610	10.2	35.2	25	8	ACI82304	Human mic
C 538	10.4	35.9	60	6	ABN49153	Human spl	Abn49153	Human spl	611	10.2	35.2	25	8	ACI26359	Human mic
539	10.4	35.9	61	3	AAAG9484	EMP-Fc fu	Aaa69484	EMP-Fc fu	612	10.2	35.2	25	8	ACI04820	Human mic
540	10.4	35.9	61	3	ABL35726	EPO mimet	AbL35726	EPO mimet	613	10.2	35.2	25	8	ACI39584	Human mic
541	10.4	35.9	64	9	ADG64605	Somatosta	Adc64605	Somatosta	614	10.2	35.2	25	8	ACK28714	Human mic
542	10.4	35.9	65	6	ABN28812	Rat spl ic	Abn28812	Rat spl ic	615	10.2	35.2	25	8	ACK28714	Human mic
543	10.4	35.9	65	6	ABN54938	Mouse spl	Abn54938	Mouse spl	616	10.2	35.2	25	8	ACI04184	Human mic
544	10.4	35.9	66	9	ADC64602	Somatosta	Adc64602	Somatosta	617	10.2	35.2	25	8	ACI96497	Human mic
C 545	10.4	35.9	67	3	AAC32336	Human sec	Aac32336	Human sec	618	10.2	35.2	25	8	ACI60065	Human mic
546	10.4	35.9	67	3	ADC64612	Somatosta	Adc64612	Somatosta	619	10.2	35.2	25	8	ACI41647	Human mic
547	10.4	35.9	70	5	AAF29244	Ligand to	Aaf29244	Ligand to	620	10.2	35.2	25	8	ACI76452	Human mic
548	10.4	35.9	71	2	AAT65354	Human ker	Aat65354	Human ker	621	10.2	35.2	25	8	ACI58807	Human mic
549	10.4	35.9	77	1	AAN22360	Gene for	Aan22360	Gene for	622	10.2	35.2	25	8	ACI16930	Human mic
550	10.4	35.9	77	1	AAQ33553	DNA seque	Aaq33553	DNA seque	623	10.2	35.2	25	8	ACH51210	DNA targe
551	10.4	35.9	79	1	AAN81448	New DNA s	Aan81448	New DNA s	624	10.2	35.2	26	3	ACH51210	DNA targe
552	10.4	35.9	79	1	AAN80972	Synthetic	Aan80972	Synthetic	625	10.2	35.2	26	8	ACH57263	DNA targe
553	10.4	35.9	79	1	AAN81355	Sequence	Aan81355	Sequence	626	10.2	35.2	26	8	ACH57263	DNA targe
554	10.4	35.9	79	1	AAN81283	Sequence	Aan81283	Sequence	627	10.2	35.2	26	9	ACH57263	DNA targe
555	10.2	35.2	20	6	AH45015	PCR prime	Aah45015	PCR prime	628	10.2	35.2	27	2	ACH57263	DNA targe
C 556	10.2	35.2	20	6	ABT13913	Human hel	Abt13913	Human hel	629	10.2	35.2	27	2	ACH57263	DNA targe
557	10.2	35.2	20	6	ABT06452	RARBeta2	Abt06452	RARBeta2	630	10.2	35.2	27	3	ACH57263	DNA targe
558	10.2	35.2	20	6	ABT06452	RARBeta2	Abt06452	RARBeta2	631	10.2	35.2	27	3	ACH57263	DNA targe
559	10.2	35.2	20	9	ADC66135	Human CFT	Adc66135	Human CFT	632	10.2	35.2	27	6	ACH57263	DNA targe
C 560	10.2	35.2	21	3	AZ77352	Human bia	Aaz77352	Human bia	633	10.2	35.2	29	6	ACH57263	DNA targe
561	10.2	35.2	21	6	ABS97827	Human NAD	Abs97827	Human NAD	634	10.2	35.2	30	2	ACH57263	DNA targe
562	10.2	35.2	21	6	ABS97828	Human NAD	AbS97828	Human NAD	635	10.2	35.2	30	2	ACH57263	DNA targe
C 563	10.2	35.2	22	2	AAQ21481	CYP synth	Aaq21481	CYP synth	636	10.2	35.2	30	4	ACH57263	DNA targe
564	10.2	35.2	22	2	AAT47391	Primer #1	Aat47391	Primer #1	637	10.2	35.2	30	4	ACH57263	DNA targe
C 565	10.2	35.2	22	6	ABS71777	Human rev	Abs71777	Human rev	638	10.2	35.2	30	6	ACH57263	DNA targe
566	10.2	35.2	23	2	AAT66337	5' primer	Aat66337	5' primer	639	10.2	35.2	31	2	ACH57263	DNA targe
567	10.2	35.2	23	6	ABS63220	Identific	Abs63220	Identific	640	10.2	35.2	31	2	ACH57263	DNA targe
C 568	10.2	35.2	23	6	ABL56402	PCR prime	AbL56402	PCR prime	641	10.2	35.2	31	9	ACH57263	DNA targe
569	10.2	35.2	23	6	ABL56399	PCR prime	AbL56399	PCR prime	642	10.2	35.2	31	9	ACH57263	DNA targe
C 570	10.2	35.2	23	6	ABL56396	PCR prime	AbL56396	PCR prime	643	10.2	35.2	32	2	ACH57263	DNA targe
571	10.2	35.2	23	9	ADE14269	Optineuri	Ade14269	Optineuri	644	10.2	35.2	32	9	ACH57263	DNA targe
C 572	10.2	35.2	24	4	AAF79515	Human G p	Aaf79515	Human G p	645	10.2	35.2	32	9	ACH57263	DNA targe
573	10.2	35.2	24	6	ABQ93701	Minimally	Abq93701	Minimally	646	10.2	35.2	33	2	ACH57263	DNA targe
574	10.2	35.2	24	6	AAD26967	BHI PCR p	Aad26967	BHI PCR p	647	10.2	35.2	33	2	ACH57263	DNA targe
C 575	10.2	35.2	24	6	ABQ05709	Oligonuel	Abq05709	Oligonuel	648	10.2	35.2	33	3	ACH57263	DNA targe
576	10.2	35.2	24	6	ABQ05750	Oligonuel	Abq05750	Oligonuel	649	10.2	35.2	33	3	ACH57263	DNA targe
C 577	10.2	35.2	24	6	ABQ00872	Oligonuel	Abq00872	Oligonuel	650	10.2	35.2	33	4	ACH57263	DNA targe
578	10.2	35.2	24	6	AAI44308	Human phy	Aai44308	Human phy	651	10.2	35.2	33	5	ACH57263	DNA targe
C 579	10.2	35.2	24	6	ABL49629	Human G p	AbL49629	Human G p	652	10.2	35.2	33	5	ACH57263	DNA targe
580	10.2	35.2	24	6	ABI86444	Capture o	Abi86444	Capture o	653	10.2	35.2	33	6	ACH57263	DNA targe
581	10.2	35.2	24	6	ABI88301	Capture o	Abi88301	Capture o	654	10.2	35.2	33	6	ACH57263	DNA targe
C 582	10.2	35.2	24	6	ABI90989	Capture o	Abi90989	Capture o	655	10.2	35.2	33	6	ACH57263	DNA targe
583	10.2	35.2	24	6	ABI86445	Capture o	Abi86445	Capture o	656	10.2	35.2	33	6	ACH57263	DNA targe
C 584	10.2	35.2	24	6	ABI84723	Capture o	Abi84723	Capture o	657	10.2	35.2	34	2	ACH57263	DNA targe
C 585	10.2	35.2	24	6	ABI90988	Capture o	Abi90988	Capture o	658	10.2	35.2	35	2	ACH57263	DNA targe
586	10.2	35.2	24	6	ABI84722	Capture o	Abi84722	Capture o	659	10.2	35.2	35	7	ACH57263	DNA targe
C 587	10.2	35.2	24	6	ABI83300	Capture o	Abi83300	Capture o	660	10.2	35.2	36	6	ACH57263	DNA targe
588	10.2	35.2	24	7	ABZ70877	Human mal	Abz70877	Human mal	661	10.2	35.2	38	8	ACH57263	DNA targe
C 589	10.2	35.2	24	8	ADA38214	Reverse p	Ada38214	Reverse p	662	10.2	35.2	39	6	ACH57263	DNA targe
590	10.2	35.2	24	9	ADG65118	Human CFT	Adg65118	Human CFT	663	10.2	35.2	40	4	ACH57263	DNA targe
C 591	10.2	35.2	24	9	ADG65118	Human CFT	Adg65118	Human CFT	664	10.2	35.2	40	6	ACH57263	DNA targe
C 592	10.2	35.2	25	3	AAA68557	Bacteriop	Aaa68557	Bacteriop	665	10.2	35.2	40	6	ACH57263	DNA targe
C 593	10.2	35.2	25	7	ABZ23287	PCR prime	Abz23287	PCR prime	666	10.2	35.2	41	5	ACH57263	DNA targe
C 594	10.2	35.2	25	8	ACI07607	Human mic	Act07607	Human mic	667	10.2	35.2	41	5	ACH57263	DNA targe
C 595	10.2	35.2	25	8	ACK17919	Human mic	Ack17919	Human mic	668	10.2	35.2	41	5	ACH57263	DNA targe
C 596	10.2	35.2	25	8	ACI59738	Human mic	Act59738	Human mic	669	10.2	35.2	41	5	ACH57263	DNA targe
C 597	10.2	35.2	25	8	ACI61052	Human mic	Act61052	Human mic	670	10.2	35.2	41	6	ACH57263	DNA targe
C 598	10.2	35.2	25	8	ACK27961	Human mic	Ack27961	Human mic	671	10.2	35.2	41	6	ACH57263	DNA targe
C 599	10.2	35.2	25	8	ACK27961	Human mic	Ack27961	Human mic	672	10.2	35.2	41	6	ACH57263	DNA targe
C 600	10.2	35.2	25	8	ACI07606	Human mic	Act07606	Human mic	673	10.2	35.2	42	2	ACH57263	DNA targe
C 601	10.2	35.2	25	8	ACK14674	Human mic	Act14674	Human mic	674	10.2	35.2	42	6	ACH57263	DNA targe
602	10.2	35.2	25	8	ACI88040	Human mic	Act88040	Human mic	675	10.2	35.2	42	7	ACH57263	DNA targe
603	10.2	35.2	25	8	ACI19123	Human mic	Act19123	Human mic	676	10.2	35.2	44	9	ACH57263	DNA targe
C 604	10.2	35.2	25	8	ACI196347	Human mic	Act196347	Human mic	677	10.2	35.2	44	9	ACH57263	DNA targe
C 605	10.2	35.2	25	8	ACK28258	Human mic	Ack28258	Human mic	678	10.2	35.2	44	9	ACH57263	DNA targe
C 606	10.2	35.2	25	8	ACK10194	Human mic	Act10194	Human mic	679	10.2	35.2	45	2	ACH57263	DNA targe
C 607	10.2	35.2	25	8	ACI191823	Human mic	Act191823	Human mic	680	10.2	35.2	45	2	ACH57263	DNA targe

C 681	10.2	35.2	46	2	AAV48399	Aav48399 P. damsel	C 754	10.2	35.2	60	6	ABN46973	Abn46973 Human spl
C 682	10.2	35.2	46	2	AAV33359	Aav33359 Primer BS	755	10.2	35.2	60	6	ABN32898	Abn32898 Human spl
C 683	10.2	35.2	46	2	AAV58401	Aav58401 Primer BS	756	10.2	35.2	60	6	ABN42766	Abn42766 Human spl
C 684	10.2	35.2	46	3	AAV57661	Aav57661 PCR prime	C 757	10.2	35.2	60	6	ABN46832	Abn46832 Human spl
C 685	10.2	35.2	47	3	AAV303527	Aav303527 Fragment	758	10.2	35.2	60	6	ABN49200	Abn49200 Human spl
C 686	10.2	35.2	47	3	AAV289012	Aav289012 Human map	759	10.2	35.2	60	6	ABN33787	Abn33787 Human spl
C 687	10.2	35.2	47	3	AAV286622	Aav286622 Human map	760	10.2	35.2	60	6	ABN33791	Abn33791 Human spl
C 688	10.2	35.2	47	3	AAV286629	Aav286629 Human map	761	10.2	35.2	60	6	ABN36323	Abn36323 Human spl
C 689	10.2	35.2	47	3	AAV286609	Aav286609 Human map	762	10.2	35.2	60	6	ABN42576	Abn42576 Human spl
C 690	10.2	35.2	47	3	AAV266750	Aav266750 Human map	763	10.2	35.2	60	6	ABN41092	Abn41092 Human spl
C 691	10.2	35.2	48	2	AAV69441	Aav69441 Human int	764	10.2	35.2	60	6	ABN458792	Abn458792 Human spl
C 692	10.2	35.2	48	2	AAV63903	Aav63903 Human int	765	10.2	35.2	60	6	ABN39736	Abn39736 Human spl
C 693	10.2	35.2	48	2	AAV17191	Aav17191 Test sequ	766	10.2	35.2	60	6	ABN49094	Abn49094 Human spl
C 694	10.2	35.2	48	6	ABK82682	Abk82682 DNA bindi	C 767	10.2	35.2	60	9	ABN87528	Abn87528 Bovine la
C 695	10.2	35.2	48	10	ABE80221	Abe80221 Duplex ol	C 768	10.2	35.2	63	2	AAQ14150	Aaq14150 Probe f63
C 696	10.2	35.2	49	2	AAAT80446	Aat80446 Hepatoma	C 769	10.2	35.2	64	2	AAQ194495	Aaq194495 Ribozyme
C 697	10.2	35.2	50	1	AAAN91943	Aan91943 Complement	C 770	10.2	35.2	64	3	AAZ507038	Aaz507038 Human gen
C 698	10.2	35.2	50	2	AAQ35511	Aaq35511 C7L-KIL d	C 771	10.2	35.2	65	2	AAV70297	Aav70297 Murine os
C 699	10.2	35.2	50	2	AAQ69716	Aaq69716 Human leu	C 772	10.2	35.2	65	2	AAV70297	Aav70297 Murine os
C 700	10.2	35.2	50	2	AAV43989	Aat43989 Octopline	C 773	10.2	35.2	65	2	AAV30440	Aav30440 3' primer
C 701	10.2	35.2	50	2	AAV64178	Aat64178 Human leu	C 774	10.2	35.2	65	2	AAV30440	Aav30440 3' primer
C 702	10.2	35.2	50	2	AAV15878	Aav15878 nos promo	C 775	10.2	35.2	65	2	ABZ28536	Abz28536 Candida g
C 703	10.2	35.2	50	2	AAV64331	Aav64331 NOS promo	C 776	10.2	35.2	65	2	ABZ28536	Abz28536 Candida g
C 704	10.2	35.2	50	2	AAV17466	Aax17466 Test sequ	C 777	10.2	35.2	65	2	ABZ28536	Abz28536 Candida g
C 705	10.2	35.2	50	4	AAAL33910	Aal33910 Human SNP	C 778	10.2	35.2	65	2	ABN28787	Abn28787 Rat splic
C 706	10.2	35.2	50	4	AAAL30163	Aal30163 Human SNP	C 779	10.2	35.2	65	2	ABN28787	Abn28787 Rat splic
C 707	10.2	35.2	50	4	AAAL34625	Aal34625 Human SNP	C 780	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 708	10.2	35.2	50	4	AAAL34625	Aal34625 Human SNP	C 781	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 709	10.2	35.2	50	6	ABK82957	Abk82957 DNA bindi	C 782	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 710	10.2	35.2	50	6	ABK82957	Abk82957 DNA bindi	C 783	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 711	10.2	35.2	50	6	ABZ01018	Abz01018 Human leu	C 784	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 712	10.2	35.2	50	6	ABZ04420	Abz04420 Human leu	C 785	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 713	10.2	35.2	50	6	ABZ01807	Abz01807 Human leu	C 786	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 714	10.2	35.2	50	6	ABZ05309	Abz05309 Human leu	C 787	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 715	10.2	35.2	50	6	ABZ05309	Abz05309 Human leu	C 788	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 716	10.2	35.2	50	6	ABZ00318	Abz00318 Human leu	C 789	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 717	10.2	35.2	50	6	ABZ01662	Abz01662 Human leu	C 790	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 718	10.2	35.2	50	6	ABZ02573	Abz02573 Human leu	C 791	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 719	10.2	35.2	50	10	AADE80496	Ade80496 Duplex ol	C 792	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 720	10.2	35.2	51	3	AAV76623	Aav76623 Human cto	C 793	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 721	10.2	35.2	51	4	AAAL27454	Aal27454 Human SNP	C 794	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 722	10.2	35.2	51	4	AAAL32109	Aal32109 Human SNP	C 795	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 723	10.2	35.2	51	4	AAAL31162	Aal31162 Human SNP	C 796	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 724	10.2	35.2	51	4	AAAL29578	Aal29578 Human SNP	C 797	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 725	10.2	35.2	51	4	AAAL28379	Aal28379 Human SNP	C 798	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 726	10.2	35.2	51	4	AAAL74294	Aal74294 Human sil	C 799	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 727	10.2	35.2	51	4	AAH90333	Aah90333 Human cto	C 800	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 728	10.2	35.2	51	4	AAH90333	Aah90333 Human cto	C 801	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 729	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 802	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 730	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 803	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 731	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 804	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 732	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 805	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 733	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 806	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 734	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 807	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 735	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 808	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 736	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 809	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 737	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 810	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 738	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 811	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 739	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 812	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 740	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 813	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 741	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 814	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 742	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 815	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 743	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 816	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 744	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 817	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 745	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 818	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 746	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 819	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 747	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 820	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 748	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 821	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 749	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 822	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 750	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 823	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 751	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 824	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 752	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 825	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl
C 753	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	C 826	10.2	35.2	65	2	ABN54772	Abn54772 Mouse spl

C 827	10	34.5	20	2	AAV28253	Aav28253 Antisense	900	10	34.5	25	8	ADA42078	Ada42078 Human sec
C 828	10	34.5	20	2	AAx18791	Aax18791 Target cy	901	10	34.5	25	8	ADA17425	Ada17425 Human sec
C 829	10	34.5	20	2	AAx23670	Aax23670 Deletion	902	10	34.5	25	8	ADA42928	Ada42928 Human sec
C 830	10	34.5	20	3	AAz49381	Aaz49381 HCMV targ	903	10	34.5	25	8	ADb23756	Adb23756 Human PRO
C 831	10	34.5	20	4	AAH25250	Aah25250 Antisense	904	10	34.5	25	9	ADb77846	Adb77846 Human sec
C 832	10	34.5	20	6	ABs98671	AbS98671 Human cyt	905	10	34.5	25	9	ADb74982	Adb74982 Human sec
C 833	10	34.5	20	6	ABi96380	Abi96380 Capture o	906	10	34.5	25	9	ADc28629	Adc28629 Human sec
C 834	10	34.5	20	6	AAJ39877	Aaj39877 Human PCR	907	10	34.5	25	9	ADc39829	Adc39829 Human sec
C 835	10	34.5	20	7	ABx78986	Abx78986 Electroni	908	10	34.5	25	9	ADc40343	Adc40343 Human sec
C 836	10	34.5	20	8	ABx281586	Abx281586 PKA regul	909	10	34.5	25	9	ADc19167	Adc19167 Human sec
C 837	10	34.5	20	9	AAE59024	Aae59024 Cytomegal	910	10	34.5	25	9	ADc34467	Adc34467 Human sec
C 838	10	34.5	20	9	ADe14503	Adel4503 HSD11B1 a	911	10	34.5	25	9	ADc29522	Adc29522 Human sec
C 839	10	34.5	20	6	ABK65538	Abk65538 Human sin	912	10	34.5	25	9	ADc29053	Adc29053 Human sec
C 840	10	34.5	21	6	ABK46947	Abk46947 COX-2 ant	913	10	34.5	25	9	ADc40938	Adc40938 Human sec
C 841	10	34.5	22	3	AAx53058	Aax53058 Human GDN	914	10	34.5	25	9	ADc19595	Adc19595 Human sec
C 842	10	34.5	22	3	AAx55585	Aax55585 Degenerat	915	10	34.5	25	9	ADc34043	Adc34043 Human sec
C 843	10	34.5	24	2	AAQ38851	Aaq38851 Sequence	916	10	34.5	25	9	ADc13113	Adc13113 Human sec
C 844	10	34.5	24	3	AAa70609	Aaa70609 Sindbis-1	917	10	34.5	25	9	ADc12565	Adc12565 Human sec
C 845	10	34.5	24	3	ABG00226	Abg00226 Oligonuc	918	10	34.5	25	9	ADd05120	Add05120 Human sec
C 846	10	34.5	24	6	ABQ10752	Abq10752 Oligonuc	919	10	34.5	25	9	ADd04126	Add04126 Human sec
C 847	10	34.5	24	6	ABQ04455	Abq04455 Oligonuc	920	10	34.5	25	9	ADd03702	Add03702 Human sec
C 848	10	34.5	24	6	ABQ10793	Abq10793 Oligonuc	921	10	34.5	25	9	ADe34954	Adel34954 Human sec
C 849	10	34.5	24	6	ABQ04424	Abq04424 Oligonuc	922	10	34.5	25	10	ADe79399	Adel79399 Human sec
C 850	10	34.5	24	6	ABQ16726	Abq16726 ccdB cyto	923	10	34.5	25	10	ADe79823	Adel79823 Human sec
C 851	10	34.5	24	6	ABL40691	Abi40691 Homo TNFR	924	10	34.5	25	10	ADe73499	Adel73499 Human sec
C 852	10	34.5	25	2	AAQ15426	Aaq15426 Vectoratt	925	10	34.5	25	10	ADe74034	Adel74034 Human sec
C 853	10	34.5	25	2	AAV07933	Aav07933 Helicobac	926	10	34.5	26	2	AAZ25364	Aaz25364 Rat DRP P
C 854	10	34.5	25	2	AAx52478	Aax52478 Forward P	927	10	34.5	27	2	AAQ47214	Aaq47214 Psi pepti
C 855	10	34.5	25	2	AAx01479	Aax01479 Primer ST	928	10	34.5	27	2	AAx98171	Aax98171 E coli D
C 856	10	34.5	25	3	AAZ92538	Aaz92538 Human Y-s	929	10	34.5	27	2	AAx42191	Aax42191 PCR prime
C 857	10	34.5	25	3	ADc78633	Adc78633 Human PRO	930	10	34.5	27	5	AAx17481	Aax17481 Tobacco m
C 858	10	34.5	25	4	AAf72636	Aaf72636 Human PRO	931	10	34.5	27	5	AAf57778	Aaf57778 Oligonuc
C 859	10	34.5	25	6	ABQ12288	Abq12288 Oligonuc	932	10	34.5	27	6	ABK87703	Abk87703 Kinased 5
C 860	10	34.5	25	6	ABQ12329	Abq12329 Oligonuc	933	10	34.5	27	6	ABL58933	Abi58933 Human tum
C 861	10	34.5	25	6	ABK28383	Abk28383 Human PRO	934	10	34.5	27	8	ACC49600	Acc49600 Beta-cong
C 862	10	34.5	25	7	ACA59461	ACA59461 Human PRO	935	10	34.5	27	9	ADc84627	Adc84627 M protein
C 863	10	34.5	25	7	ACA58558	ACA58558 PCR prime	936	10	34.5	27	9	ADe62031	Adel62031 PCR prime
C 864	10	34.5	25	7	ACA60265	ACA60265 Human sec	937	10	34.5	28	2	AAZ30900	Aaz30900 HIV-1 vpr
C 865	10	34.5	25	7	ACD07666	AcD07666 Novel hum	938	10	34.5	28	10	ADe83593	Adel83593 CHREBP mu
C 866	10	34.5	25	7	ABX71714	Abx71714 Human sec	939	10	34.5	28	10	ADe83592	Adel83592 CHREBP mu
C 867	10	34.5	25	7	ACH07045	Ach07045 Human sec	940	10	34.5	29	2	AAx197242	Aax197242 Hepatitis
C 868	10	34.5	25	7	ABX96282	Abx96282 Human sec	941	10	34.5	29	2	ABX13988	Abx13988 Decoy-rib
C 869	10	34.5	25	7	ACA05603	ACA05603 Human sec	942	10	34.5	29	2	AAQ57988	Aaq57988 Sequence
C 870	10	34.5	25	7	ACD20270	AcD20270 Human sec	943	10	34.5	30	2	AAQ97758	Aaq97758 Primer #1
C 871	10	34.5	25	7	ACA55074	ACA55074 Secreted	944	10	34.5	30	3	AAA88141	Aaa88141 Mouse (ba
C 872	10	34.5	25	8	ADc19908	Adc19908 Human sec	945	10	34.5	30	5	AAx06528	Aax06528 Mouse mic
C 873	10	34.5	25	8	ADc29525	Adc29525 Human sec	946	10	34.5	30	6	ABX68071	Abx68071 Novel Hel
C 874	10	34.5	25	8	ADa18382	Ada18382 Human sec	947	10	34.5	30	6	ABK91841	Abk91841 TGRP/Mg21
C 875	10	34.5	25	8	ACD67055	AcD67055 Human sec	948	10	34.5	30	7	ACA99430	ACA99430 Enzyme DN
C 876	10	34.5	25	8	ACI87429	AcI87429 Human mic	949	10	34.5	31	2	AAV032556	Aav032556 Probe b33
C 877	10	34.5	25	8	ACK14978	Ack14978 Human mic	950	10	34.5	31	3	AAZ36581	Aaz36581 D. farina
C 878	10	34.5	25	8	ACI74215	AcI74215 Human mic	951	10	34.5	31	4	AAH97186	Aah97186 Human Chk
C 879	10	34.5	25	8	ACI18794	AcI18794 Human mic	952	10	34.5	31	4	AAH97151	Aah97151 Human Chk
C 880	10	34.5	25	8	ACI14714	AcI14714 Human mic	953	10	34.5	31	4	AAH97177	Aah97177 Human Chk
C 881	10	34.5	25	8	ACI96627	AcI96627 Human mic	954	10	34.5	31	4	ABK06334	Abk06334 Human NOG
C 882	10	34.5	25	8	ACI33391	AcI33391 Human mic	955	10	34.5	31	4	ABK06618	Abk06618 Human NOG
C 883	10	34.5	25	8	ACK10665	Ack10665 Human mic	956	10	34.5	31	4	ABK06494	Abk06494 Human NOG
C 884	10	34.5	25	8	ACK02514	Ack02514 Human mic	957	10	34.5	31	4	ABK06479	Abk06479 Human NOG
C 885	10	34.5	25	8	ACI04864	AcI04864 Human mic	958	10	34.5	31	4	ABK08755	Abk08755 Human CD2
C 886	10	34.5	25	8	ACI74214	AcI74214 Human mic	959	10	34.5	31	4	ABK06409	Abk06409 Human NOG
C 887	10	34.5	25	8	ACI74499	AcI74499 Human mic	960	10	34.5	31	4	ABK06607	Abk06607 Human NOG
C 888	10	34.5	25	8	ACI94439	AcI94439 Human mic	961	10	34.5	31	4	ABK06730	Abk06730 Human NOG
C 889	10	34.5	25	8	ACT26164	Act26164 Human mic	962	10	34.5	31	4	ABL48137	Abi48137 Human GRI
C 890	10	34.5	25	8	ACI35563	AcI35563 Human mic	963	10	34.5	31	4	ABL48039	Abi48039 Human GRI
C 891	10	34.5	25	8	ACI86332	AcI86332 Human mic	964	10	34.5	31	4	ABL47967	Abi47967 Human GRI
C 892	10	34.5	25	8	ACI76988	AcI76988 Human mic	965	10	34.5	31	4	AAI30431	Aai30431 Human sin
C 893	10	34.5	25	8	ACI41795	AcI41795 Human mic	966	10	34.5	31	6	ABK69577	Abk69577 Der HW-m
C 894	10	34.5	25	8	ACI43216	AcI43216 Human PRO	967	10	34.5	31	6	ABK21221	Abk21221 Human ERG
C 895	10	34.5	25	8	ADa16357	Ada16357 Human sec	968	10	34.5	31	6	ABK21846	Abk21846 Human ERG
C 896	10	34.5	25	8	ADa42502	Ada42502 Human sec	969	10	34.5	31	6	ABK21763	Abk21763 Human ERG
C 897	10	34.5	25	8	ADc23394	Adc23394 Human PRO	970	10	34.5	31	6	ABK21526	Abk21526 Human ERG
C 898	10	34.5	25	8	ADa16781	Adal6781 Human sec	971	10	34.5	31	6	ABK21816	Abk21816 Human ERG
C 899	10	34.5	25	8	ADA13210	Ada13210 Human sec	972	10	34.5	31	6	ABK21784	Abk21784 Human ERG

C 973 10 34.5 31 6 ABK59591 Human CLC
C 974 10 34.5 31 6 ABK60175 Human CLC
C 975 10 34.5 31 6 ABK60218 Human CLC
C 976 10 34.5 31 7 ACA08736 Necrosis
C 977 10 34.5 31 7 ACA08736 Necrosis
C 978 10 34.5 31 7 ACA08519 Necrosis
C 979 10 34.5 31 7 ACA08428 Necrosis
C 980 10 34.5 31 7 ABZ64323 Human H-R
C 981 10 34.5 31 7 ABZ65625 Human HER
C 982 10 34.5 31 7 ABZ66411 Human HER
C 983 10 34.5 31 7 ABZ66193 Human HER
C 984 10 34.5 31 7 ABZ63649 Human H-R
C 985 10 34.5 31 7 ABZ65802 Human HER
C 986 10 34.5 31 7 ABZ66429 Human HER
C 987 10 34.5 31 7 ABZ63855 Human H-R
C 988 10 34.5 31 7 ABZ65950 Human HER
C 989 10 34.5 31 7 ABZ66027 Human HER
C 990 10 34.5 31 7 ABZ64429 Human H-R
C 991 10 34.5 31 7 ABZ64440 Human H-R
C 992 10 34.5 31 7 ABZ66392 Human HER
C 993 10 34.5 31 7 ABZ62244 Human K-R
C 994 10 34.5 31 7 ABZ63310 Human K-R
C 995 10 34.5 31 7 ABZ66208 Human HER
C 996 10 34.5 31 7 ABZ66420 Human HER
C 997 10 34.5 31 7 ABZ62308 Human K-R
C 998 10 34.5 31 7 ABZ63853 Human H-R
C 999 10 34.5 31 7 ABZ65850 Human HER
C1000 10 34.5 31 7 ABZ65732 Human HER

ALIGNMENTS

RESULT 1
ID AAA70827 standard; RNA; 29 BP.
XX AC
XX AAA70827;
XX 27-APR-2001 (first entry)
XX Molecular interaction site RNA #27.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Synthetic.
XX WO9558947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Claim 235; Page 235; 405pp; English.

XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of

CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of a second
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; and (g) 3
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAAUAUACUAGUACAGAAAAAUC (11). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX Sequence 29 BP; 4 A; 4 C; 5 G; 0 T; 5 U; 11 Other;
SQ

Query Match 62.1%; Score 18; DB 3; Length 29;
Best Local Similarity .100.0%; Pred. No. 2.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCUUNNGUAGCCCNANGNG 27
DB 4 GAUUCUUNNGUAGCCCNANGNG 27

RESULT 2
AAA70829
ID AAA70829 standard; RNA; 29 BP.
XX AC
XX AAA70829;
XX 27-APR-2001 (first entry)
XX Molecular interaction site RNA #29.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Mus sp.
XX WO9558947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Claim 235; Page 235; 405pp; English.

XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds

CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAAUACUAGUUUACAGAAAUC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX
 SQ Sequence 42 BP; 13 A; 7 C; 7 G; 0 T; 15 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 42;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 4 GAUUCUUUNNGUAAGCCCNANGNG 27
 ||| |||| ||||| ||||| |||||
 Db 7 GAUUCUUUNNGUAAGCCCAAGG 30

RESULT 7
 AAA71123
 ID AAA71123 standard; DNA; 42 BP.
 AC AAA71123;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Molecular interaction site DNA #129.
 XX
 KW Modulator; identification; molecular interaction; virtual library; ss.
 OS Unidentified.
 XX
 PN W09958947-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 12-MAY-1999; 99WO-US010361.
 XX
 PR 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 XX
 DR WPI; 2000-086439/07.
 XX
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 PS Example 7; Fig 125; 405pp; English.

CC This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24

CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAAUACUAGUUUACAGAAAUC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX
 SQ Sequence 42 BP; 9 A; 6 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 42;
 Best Local Similarity 54.2%; Pred. No. 2.2;
 Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 4 GAUUCUUUNNGUAAGCCCNANGNG 27
 ||| |||| ||||| ||||| |||||
 Db 7 GATTCTTTTGTAAAGCCCTAGGG 30

RESULT 8
 AAA71113
 ID AAA71113 standard; RNA; 42 BP.
 AC AAA71113;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Molecular interaction site RNA #189.
 XX
 KW Modulator; identification; molecular interaction; virtual library; ss.
 OS Unidentified.
 XX
 PN W09958947-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 12-MAY-1999; 99WO-US010361.
 XX
 PR 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 XX
 DR WPI; 2000-086439/07.
 XX
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 PS Example 7; Fig 122; 405pp; English.

CC This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24

nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACACAUAUUCUAGUUAUCAGAAAAUUC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

Sequence 42 BP: 12 A; 7 C; 6 G; 0 T; 17 U; 0 other;
xx

```
Query Match      62.1%; Score 18; DB 3; Length 42;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

QY 4 GAUNCUUNNGUAAGCCCNANG 27
|||||
Dd 7 GATUCUUNNGUAAGCCCUACGG 30
|||||

RESULT 9	
AAA71124	
ID	AAA71124 standard; DNA; 42 BP.
XX	
AC	AAA71124;
XX	
XX	
DT	27-APR-2001 (first entry)
XX	
DE	Molecular interaction site DNA #130.
XX	
KW	Modulator; identification; molecular interaction; virtual library; ss.
XX	
OS	Unidentified.
XX	
PN	WO9958947-A2.
XX	
PD	18-NOV-1999.
XX	
PF	12-MAY-1999; 99WO-US010361.
XX	
PR	12-MAY-1998; 98US-00076404.
PR	12-MAY-1998; 98US-0085092P.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Eker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI	Hofstadler S, Mcneil J;
XX	
DR	WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.

XX PS Example 7: Fig 125: 405pp: English:

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating *in silico* a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary

structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUUACAUAUACUGUUUACAGAAAUAUC (II'). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

Sequence 42 BP: 11 A; 10 C; 7 G; 14 T; 0 U; 0 Other; XX

Query Match	62.1%	Score 18	DB 3	Length 42
Best Local Similarity	54.2%	Pred. No. 2.2		
Matches 13	Conservative 5	Mismatches 6	Indels 0	Gaps 0

Qy

4 GAUNCUUUNNGUAAGCCCNANGG 27
||| : | : |||
Dd

7 GATCCTTTCTGTAAGCCCTACGGG 30
|||| :

```

RESULT 10
AAA71132
ID AAA71132 standard; RNA; 42 BP.
XX
XX AAA71132;
XX AC
XX AC
XX 27-APR-2001 (first entry)
XX DT
XX XX
XX Molecular interaction site RNA #201.
XX DE
XX DE
XX DE
XX Modulator: identification: molecular interaction; virtual library; ss.
KW

```

XX	
OS	Unidentified.
XX	
PN	WO9958947-A2.

XX PD 18-NOV-1999.

XX	12-MAY-1999;	99WO-US010361.
XX	12-MAY-1998;	98US-00076404.
XX	12-MAY-1998;	98US-0085092P.
XX	(ISIS-) ISIS PHARM INC.	
XX	Ekker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;	
XX	Hofstadler S, Mcneil J;	
XX	WPI; 2000-086439/07.	
XX	Identifying compounds which modulate activity of target biomolecules,	
XX	used to provide compounds which can be used as pharmacological,	
XX	agricultural and industrial compounds.	

XX PS Example 7: Fig 126; 405pp; English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first site of a first

CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAAUACUAGUUUACAGAAAAC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
xx
SQ Sequence 42 BP; 12 A; 7 C; 6 G; 17 T; 0 U; 0 Other;

```
Query Match      62.1%;   Score 18;   DB 3;   Length 42;  
Best Local Similarity 54.2%;   Pred. No. 2.2;  
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0  
  
QY    4 GAUUCUUUNNGUAAGCCCNANGNG 27  
      ||::|||:  
Db    7 GATCTTTTGTGAACCCCTACGGG 30
```

```

RESULT 14
AAA71119
ID AAA71119 standard; DNA; 42 BP.
XX XX
AC AAA71119;
XX XX
DT 27-APR-2001 (first entry)
XX XX
DE Molecular interaction site DNA #125.
XX XX
KW Modulator; identification; molecular interaction; virtual library; ss

```

OS	Unidentified.
XX	
XX	WO9958947-A2.
PN	
XX	
XX	18-NOV-1999.
PD	
XX	
XX	12-MAY-1999; 99WO-US010361.
PF	
XX	
XX	12-MAY-1998; 98US-00076404.
PR	
PR	12-MAY-1998; 98US-0085092P.
XX	
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
XX	Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI	Hoistadler S, Mcneil J;
PI	
XX	
XX	WPI; 2000-086439/07.
DR	
XX	
XX	Identifying compounds which modulate activity of target biomolecules.
PT	to provide compounds which can be used as pharmacological,
PT	agricultural and industrial compounds.
XX	
XX	
PS	Example 7: Fig 135: 405pp: English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4

CC or industrial compounds
XX Sequence 44 BP; 7 A; 4 C; 5 G; 0 T; 6 U; 22 Other;
SQ Query Match 62.1%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 8 GAUNCUUNNGUAGCCCNANGNG 31
RESULT 23
AAA71125
ID AAA71125 standard; RNA; 44 BP.
XX AC AAA71125;
XX DT 27-APR-2001 (first entry)
XX Molecular interaction site RNA #194.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Unidentified.
XX WO9958947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Example 7; Fig 126; 405pp; English.
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; and (f) 4
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAUAAUACUUAACAAAAC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds

XX Sequence 44 BP; 7 A; 4 C; 5 G; 0 T; 6 U; 22 Other;
SQ Query Match 62.1%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 8 GAUNCUUNNGUAGCCCNANGNG 31
RESULT 24
AAA71133
ID AAA71133 standard; RNA; 44 BP.
XX AC AAA71133;
XX DT 27-APR-2001 (first entry)
XX Molecular interaction site RNA #202.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Unidentified.
XX WO9958947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Example 7; Fig 127; 405pp; English.
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; and (g) 3
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAUAAUACUUAACAAAAC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds

SQ Sequence 44 BP; 7 A; 4 C; 5 G; 0 T; 6 U; 22 Other;
Query Match 62.1%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUNCUUUNGUAGCCCNANGNG 27
|||||
Db 8 GAUNCUUUNGUAGCCCNANGNG 31
|||||

RESULT 25
AAA70826
ID AAA70826 standard; RNA; 45 BP.
XX
AC AAA70826;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #26.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Rattus sp.
XX
PN WO9558947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Claim 22; Page 232; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUACUACUACGAGAAAUUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 45 BP; 14 A; 7 C; 9 G; 0 T; 15 U; 0 Other;

SQ Sequence 44 BP; 7 A; 4 C; 5 G; 0 T; 6 U; 22 Other;
Query Match 62.1%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUNCUUUNGUAGCCCNANGNG 27
|||||
Db 8 GAUNCUUUNGUAGCCCNANGNG 31
|||||

RESULT 26
AAA70825
ID AAA70825 standard; RNA; 45 BP.
XX
AC AAA70825;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #25.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Mus sp.
XX
PN WO9558947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Claim 22; Page 232; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUACUACUACGAGAAAUUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 45 BP; 14 A; 7 C; 9 G; 0 T; 15 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 45;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUNCUUUNGUAGCCCNANGNG 27
|||||
Db 21 GAUUCUUUUUGAAGCCCAAGGG 44
|||||

RESULT 26
AAA70825
ID AAA70825 standard; RNA; 45 BP.
XX
AC AAA70825;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #25.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Mus sp.
XX
PN WO9558947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Claim 22; Page 232; 405pp; English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACACAUACUACUACGAGAAAUUC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds
Sequence 45 BP; 14 A; 7 C; 9 G; 0 T; 15 U; 0 Other;

22 GAUCCUUCUGUAAGCCUACGGG 45

Db 22 GAUCCUUCUGUAAGCCUACGGG 45

RESULT 33
AAA71095
ID AAA71095 standard; DNA; 46 BP.
XX AC
XX AAA71095;
DT 27-APR-2001 (first entry)
XX DE Molecular interaction site DNA #118.
XX DE Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, Mcneil J;
XX DR WPI; 2000-086439/07.
XX DR Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 121; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX CC internal loop region; (c) 4 nucleotides forming a first side of a second
XX CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC nucleotides forming a second side of the second ds region; and (g) 3
XX CC nucleotides forming a second side of the internal loop region; and (2) a purified
XX CC nucleotides forming a second side of the first ds region; (f) 4
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAUUAUCUUAAGCCUACGGG (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds

Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. NO. 2.2;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUCCUUNGUAGCCUACGGG 27
|||:::|:|||||
Db 22 GATCCTTCGTGTAAGCCCTACGGG 45

RESULT 34
AAA71106
ID AAA71106 standard; RNA; 46 BP.
XX AC
XX AAA71106;
DT 27-APR-2001 (first entry)
XX DE Molecular interaction site RNA #182.
XX DE Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, Mcneil J;
XX DR WPI; 2000-086439/07.
XX DR Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 122; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX CC internal loop region; (c) 4 nucleotides forming a first side of a second
XX CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC nucleotides forming a second side of the second ds region; and (g) 3
XX CC nucleotides forming a second side of the internal loop region; and (2) a purified
XX CC nucleotides forming a second side of the first ds region; (f) 4
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAUUAUCUUAAGCCUACGGG (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds

Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 75.0%; Pred. NO. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUCCUUNGUAGCCUACGGG 27
|||:::|:|||||
Db 22 GAUCCUUNGUAGCCUACGGG 45

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RESULT 35
AAA71107
ID AAA71107 standard; RNA; 46 BP.
XX
XX
AC AAA71107;
XX
XX
DT 27-APR-2001 (first entry)
XX
XX
DE Molecular interaction site RNA #183.
XX
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
XX
OS Unidentified.
XX
XX
PN WO9958947-A2.
XX
XX
PD 18-NOV-1999.
XX
XX
PF 12-MAY-1999; 99WO-US010361.
XX
XX
PR 12-MAY-1998; 98US-00076404.
XX
XX
PR 12-MAY-1998; 98US-0085092P.
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PA (ISIS-) ISIS PHARM INC.
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PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX
DR WPI; 2000-086439/07.
XX
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
XX
PS Example 7; Fig 122; 405pp; English.
XX
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
CC ds region; (d) 4 or 5 nucleotides forming a second side of a second
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAAUAUCUUAAGUUAAGCCCNANGNG 27
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
XX
SQ Sequence 46 BP; 14 A; 7 C; 9 G; 0 T; 16 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUUCUUUNGUUAAGCCCNANGNG 27
Db 22 GAUUCUUUNGUUAAGCCCNANGNG 45
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RESULT 36
AAA71109
ID AAA71109 standard; RNA; 46 BP.
XX
XX
AC AAA71109;
XX
XX
DT 27-APR-2001 (first entry)
XX
XX
DE Molecular interaction site RNA #185.
XX
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
XX
OS Unidentified.
XX
XX
PN WO9958947-A2.
XX
XX
PD 18-NOV-1999.
XX
XX
PF 12-MAY-1999; 99WO-US010361.
XX
XX
PR 12-MAY-1998; 98US-00076404.
XX
XX
PR 12-MAY-1998; 98US-0085092P.
XX
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX
DR WPI; 2000-086439/07.
XX
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
XX
PS Example 7; Fig 122; 405pp; English.
XX
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
CC ds region; (d) 4 or 5 nucleotides forming a second side of a second
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAAUAUCUUAAGUUAAGCCCNANGNG 27
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
XX
SQ Sequence 46 BP; 9 A; 11 C; 9 G; 0 T; 17 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUUCUUUNGUUAAGCCCNANGNG 27
Db 22 GAUUCUUUNGUUAAGCCCNANGNG 45
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RESULT 37


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XX AAA71096;
AC 27-APR-2001 (first entry)
XX Molecular interaction site DNA #119.
DE Modulator; identification; molecular interaction; virtual library; ss.
XX Unidentified.
XX WO9958947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Example 7; Fig 121; 405pp; English.
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; and (f) 3
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUACUAGUUACAGAAAUC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds
XX
SQ Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;
Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. No. 2.2;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 22 GATTCCTTTTGTAGCCCTAGGGG 45
RESULT 40
AAA71099
ID AAA71099 standard; DNA; 46 BP.
XX
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AC AAA71099;
XX 27-APR-2001 (first entry)
XX Molecular interaction site DNA #122.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Unidentified.
XX WO9958947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Example 7; Fig 121; 405pp; English.
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; and (f) 3
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUACUAGUUACAGAAAUC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds
XX
SQ Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;
Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. No. 2.2;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 22 GATTCCTTTTGTAGCCCTAGGGG 45
Search completed: April 18, 2004, 08:03:33
Job time : 217.667 secs
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